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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 26, 2005, 03:05:20 ; Search time 2327 Seconds (without alignments) 8245.924 Million cell updates/sec Run on:

1 atgatgagtcctgcccagtt......gcaccaagctggaaatcaaa 396 US-10-010-942B-1 396 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

9416466 Total number of hits satisfying chosen parameters:

4708233 segs, 24227607955 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

GenBmbl:*

1: 90 ba:*

90 ba:*

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90 ba:*

90 pa:*

90 pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AX458138 Sequence	M20830 Mouse IqMk	AY571288 Mus muscu	AF045492 Mus muscu	AF045493 Mus muscu	BC028925 Mus muscu	M17722 Mouse Ig ac	CQ829526 Sequence	D17386 Mus sp. mRN	L26541 Mouse immun	AR452630 Sequence	AR452631 Sequence	AF157686 Mus muscu	Z17401 Mus musculu	BC031498 Mus muscu	AR477534 Sequence	AR477539 Sequence	AR532506 Sequence	AR532511 Sequence
ΩI	AX458138	MUSIGKCLM) AY571288) AF045492) AF045493) BC028925	MUSICKCJ	CQ829526	MUSIFC) MUSIGMVA	AR452630	AR452631) AF157686	MMIGKEAD) BC031498	AR477534	AR477539	AR532506	AR532511
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å Query Match Length DB	396	428	930	393	393	1034	393	717	927	423	393	393	396	408	1008	426	426	426	426
Query Match	100.0	98.0	97.2	96.0	96.0	94.5	93.6	93.6	92.3	91.5	91.2	91.2	90.8	7.06	85.9	84.7	84.7	84.7	84.7
Score	396	388	384.8	380.2	380.2	374.4	370.8	370.6	365.6	362.4	361	361	359.4	359.2	340	335.4	335.4	335.4	335.4
Result No.	-	7	m	4	S	9	7	œ	6	10	11	12	13	14	15	16	c 17	18	c 19

AX208063 Sequence AX208069 Sequence 219575 Mussculus AP086602 Mus musculus AP086602 Mus musculu L22655 Rat anti-ac AP143910 Mus muscul BD244502 Cells exp AR454911 Sequence A07556 DNA Sequence L3475 Mus muscul A22353 Mus muscul L43543 Mus muscul L43543 Mus muscul L43543 Mus muscul L43544 Mus muscul L43544 Mus muscul L43544 Mus musculu L43544 Mus musculu L43544 Mus musculu	0000
6 AX208063 10 MMRIGLC 10 MMRIGLC 10 MUSIGKVRA 10 RAJIGK132A 10 AF143910 6 AR454911 6 AR454911 6 AR454911 6 AR454911 10 MUSABLIGHT 10 MUSIGLDB 10 AF486644 10 MWIGLDB 10 AF486644 10 MWIGLDB 10 AF486644 10 MWIGLDB 10 MWIGLDB	10 MUSIGKCOJ 10 MUSIGKGOJ 10 MUSIGKSG2 110 AYS56405 12 AF064776 6 AR131300
426 426 426 4605 336 336 336 336 338 338 338 338 338 338	339 339 336 336 360
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3335.4 3333.6 3333.6 333.6 333.6 3322.2 3322.2 3322.2 319 319 3119 3119 3117.4	315.8 315.8 315.8 315.8
0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1 0 T C E T T T

ALIGNMENTS

linear PAT 08-JUL-2002	Craniata; Vertebrata; Buteleostomi; Sciurognathi: Muridae: Murinae: Mus	amyloid peptide		TNGYVVMTQTPLTLSVTIGQPASISCK NSKLDSGVPDRFTGSGSGTDFTLKISR	; Length 396; 20; Indels 0; Gaps 0;	CTGGATTCGGGAAACCAACGT 60 	TACCATTGGACAACCAGCCTCC 120
AX458138 396 bp DNA AX458138 1:21724896	Mus musculus (house mouse) Mus musculus Eukaryota, Metazoa; Chordata; Craniata; Mammalia: Eutheria: Rodentia: Sciurognat	and Yednos that reco	- 2CX	/note="unnamed protein product" /codom start=1 /protein_id="CAD38344.1" /pb.exef="GAD38344.1" /db.xref="GAD38344.1" /translation="MMSPAQFLFILVI.WIRETNGYVVMTQTPLTLSVTIGQPASISCK SSQSLLDSDGKTYLNWLLATDGPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISR IEAEDIGLYYCMQGTHPPRTFGGGTKLBIK	<pre>ide 160 100.0%; Score 396; DB 6 Similarity 100.0%; Pred. No. 4.7e-1 6; Conservative 0; Mismatches</pre>	1 ATGATGAGICCTGCCCAGITCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGT 	TATGITGIGATGACCCAGACTCCACTCACTITGTCGGTTACCATTGGACAACCAGCCTCC 120
Ž Ö z	KEYWORDS SOURCE ORGANISM N	REFERENCE AUTHORS TITLE JOURNAL	PEATURES BOULCE		sig_peptide ORIGIN Query Match Best_Local Sim Matches 396;	රු සි	Qy 61

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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. B. (bases 1 to 930)

8 Wang, H.L., Lee, C.H. and Hsu, H.T. Molecular Cloning and Sequencing of Heavy and Light Chain cDNAs from Papaya ringspot and Cymbidium mosaic viruses-Specific Monoclonal Antibodies

1. Zhi Wu Bing Li Xue Hui Kan 13 (2004) In press

2. (bases 1 to 930)

8 Wang, H.L., Lee, C.H. and Hsu, H.T.

5 Unect Submission

1. Submitted (11-MAR-2004) Graduate Institute of Biology Science, National Kaohsiung Normal University, 116, Ho Ping 1Rd, Kaohsiung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein id="AAT74922.1"
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LANNFYPKDINVFWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY571288 930 bp mRNA linear ROD 21-JUL-2004 Mus musculus anti-CMV coat protein monoclonal antibody CymMV-L 23 immunoglobulin light chain variable region mRNA, complete cds.
                                                                                                                                        93 GATGTTGTGATGACCCAGACTCCACTCACTTTGTTGTTACCATTGGACAACCAGCCTCC 152
                                                                                                                                                                                                                                                                                                     153 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAGACATATTTGAATTGG 212
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CymMV-L 23 immunoglobulin light chain variable region"
                                               33 ATGATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGT
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AY571288.1 GI:50346341
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AY571288
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light chain; immunoglobulin-kappa.
Mus musculus (house mouse)
Mus musculus
TATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 120
                                            180
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Draft entry and computer-readable sequence [1] kindly submitted by R.Kofler 28-JUL-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 428)
Kofler, R., Strohal, R., Balderas, R.S., Johnson, M.E., Noonan, D.J., Duchosal, M.A., Dixon, F.J. and Theofilopoulos, A.N.
Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA
                                                                TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC
                                                                                                                               Gaps
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33. .>428
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J. Clin. Invest. 82 (3), 852-860 (1988)
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1. ->428
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2 (bases 1 to 393)
O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D.
Direct Submission
Submitted (02-FBB-1998) Biochemistry, Tufts University School
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                      Length 393;
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Pred. No. 8.5e-115;
0; Mismatches 8;
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    .393
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98.0%;
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                                                                                                                                                                                                                                                                                                                                                                     63 GATGTTGTGATGACCCCAGACTCCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 122
                                                                                                                                                                                                                                                                           ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAAAAGACATATTTGAATTGG 180
                                                                                                                                                                                                                                                                                                                                                  TIGITACAGAGGCCAGGCCAGICTCCCAAAGCGCCTAAICTAICTGGTGTTTAAACTGGAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 AGCAGAGAGGCTGAGGATTTGGGAATTTATTACTGCTGGCAAGGTACACTTTTCCT 362
                                                                                                                                                                                                 TATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 120
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O'Connor, K.C., Farrell, T.P., Morikawa, A. and Stollar, B.D. Anti-DNA antibodies of normal mice immunized with poly(dC) are structurally similar to natural autoantibodies
                                                                                                                            9
                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'CONDO'K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
Direct Submission
Submitted (02-FBE-1998) Biochemistry, Tufts University School of
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
Location/Qualifiers
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                                                                                                                          1 ATGATGAGTCCTGCCCAGTTCCTGTTAGTGCTCTGGATTCGGGAAACCAACGGT
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                                                   Score 384.8; DB 10;
Pred. No. 2.7e-116;
0; Mismatches 7;
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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/chromosome="6"
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1. .>393
/gene="1gK"
                                                   Query Match
Best Local Similarity 98.2%;
Matches 389; Conservative
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleron, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.B., Eromatein, M.J., Usdin, T.B., Toshiyuti, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramaon, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villahon, D.K., Muzny, D.M., Sodergen, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M. Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M. I., Skalska, U., Smailus, D.E., Schnert, A., Schein, J. E., Jones, S.J. and Marra, M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
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/product=u0hknown (protein for MGC:25820)"
/product=u1 id="AAH28925.2"
/db_xref="G1:54035189"
/tb_xref="G1:54035189"
/tb_xref="G1:54035189"
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Tissue Procurement: Jeffrey E. Green, M.D.

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center

Center code: BCM-HGSC

Web site: http://www.hgsc.bcm.tmc.edu/cdna/

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,

Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,

A.N., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 30 Row: m Column: 13

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers

1. .1034

/organism="Musm musculus"
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/clone="MGC:25820 IMAGB:4164906"
/tissue_type="Salivary gland, 10 week old female mouse"
/clone_lib="MCI CGAP_SG2"
/lab_host="DH10B"
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Contact: MGC help desk
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Best Local Similarity 98.2%; Pred. No. 7.8e-113;
Matches 389; Conservative 0; Mismatches 6;
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/strain="FVB/N"
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Direct Submission
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/db_xref="G1:2906070"
/tb_xref="G1:2906070"
/tb_xref="G1:2906070"
/tb_xref="G1:2006070"
/tb_xref="G1:200607
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 1034)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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/product="anti-poly(dC) monoclonal antibody kappa light
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Mus musculus CDNA clone MGC:25820 IMAGE:4164906, complete cds.
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0; Mismatches 8; Indels
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chromosome="6"
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                          etrain="C57BL/6"
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Matches 385; Conservative
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/gene="IgK"
358. .>393
/gene="IgK"
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/gene="IgK"
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/gene="IgK"
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Bispecific anti-idiotype/anti-CD3 antibody therapy of murine B cell
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Weiner, G.J. and Kaminski, M.S. Anti-idiotypic antibodies recognizing stable epitopes limit the emergence of idiotype variants in a murine B cell lymphoma J. Immunol. 144 (6), 2436-2445 (1990)
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                                                                                                                                                                                                                                                        TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 300
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The role of T cell activation in anti-CD3 x antitumor bispecific
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Mouse immunoglobulin light chain variable region.
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V-region; immunoglobulin; light chain.
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J. Immunol. 152 (5), 2385-2392 (1994)
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/organism="Mus musculus"
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/isolate="MS9A6"
/db_xref="taxon:10090"
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Weiner, G.J. and Hillstrom, J.R.
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/cell_line="T3C"
/cell_type="B-cell"
12. 27
88. .423
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Molecular cloning and nucleotide sequences of heavy and light chain
genes of a monoclonal antibody to potato virus Y coat protein
Ann. Phytopathol. Soc. Jpn. 60, 600-607 (1994)
2 (bases 1 to 927)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MMSPAQPLFLLVLCIRETWGDVVMTQTPLTLSVTIGQPASISCK
ssqsllvsdgktvltdkpeqgsprkliylvskldsgvpdrftgsgsgtdptlkisr
veaedigvyvcwqsthppftrgsgtkleikabaaptvsipppssedlisgasvvcp
lnnfypkdinvkwkidgsbrqwcvnswtdqdskdstysmsstlsltkdeyerhnsyt
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                                                                                   241 GGAGTCCCTGACAGGTTCACTGGCAGTGGGATCAGGGACGGATTTCACACTGAAAATCAGG 300
                                                                                                                                        304 AGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCTCGG 363
                                                                                                                                                            Direct Submission
Submitted (109-A01-1993) Kazusato Ohshima, Faculty of Agriculture,
Saga University, Laboratory of Plant Viology; 1 Honjo-machi, Saga,
Saga 840, Japan (Tel:81-952-24-5191(ex.2730), Fax:81-952-22-6274)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamaalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mamaes 1 to 927)

Ohebima K., Matsuura, A., Nakaya, T., Shikata, E., Kikuchi, K. and
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                                                             GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:10095"
/note="42C07 monoclonal antibody-secreting hybridoma"
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/product="immunoglobulin light chain"
/product="immAn64204.1"
/db_xref="GI:1794158"
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Pred. No. 6.5e-110;
0; Mismatches 19;
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kappa chain
to potato virus Y coat protein"
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                                                                                                                                                                                                                                            organism="Mus sp."
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Best Local Similarity 95.2%;
Matches 377; Conservative
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Sato, K., Adachi, H. and Yabuta, N.
Humanized antibody against human tissue factor (TF) and process
production of the humanized antibody
Patent: US 6677436-A 17 13-JAN-2004;
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AR452631
AR452631.1 GI:42684512
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Sato, K., Adachi, H. and Yabuta, N.
Humanized antibody against human tissue factor (TF) and process production of the humanized antibody
Patent: US 6677436-A 16 13-JAN-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAATCAACGGTGAT
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                                                 Score 362.4; DB 10; Length 423; Pred. No. 7e-109; 0; Mismatches 21; Indels 0;
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94.9%; Pred. No. 2e-108;
iive 0; Mismatches 20
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Sequence 16 from patent US 6677436.
AR452630.1 GI:42684511
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/organism="unknown"
/mol_type="genomic DNA"
 /note="Ig light chain"
                                                 Query Match
Best Local Similarity 94.7%;
Matches 375; Conservative
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Matches 373, Conservative
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J. Exp. Med. 177 (5), 1317-1330 (1993) 93240113
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/mol_type="mRNA"
/strain="BALB/c"
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/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="B-cell"
/tissue_type="Liver"
/dev_stage="Fetus"
13. 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="FL-31
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Best Local Similarity 94.2%;
Matches 373; Conservative
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Medina, C.A.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AaD41897.1"
/db_xref="G1:5306068"
/translation="MSPAPELPLYLWIRETSGDVWTQTPLTLSVTIGQPASISCKS
SQSLLDSDGETYLMHLQRPGQSPKRLIYWSKLDSGVPDRFFGSGSGTDFTLKISRV
BAEDLGVYYCWQGTHPPPFTFGSGTKLEIKR"
AF157686 396 bp mRNA linear ROD 30-MAY-2000 Mus musculus immunoglobulin kappa light chain variable region mRNA,
                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I bases 1 to 396)
Park, O.Y., Jin, Y.H., Lee, M., Shin, H.J., Kim, H.I., Cho, H., Yun, C.W., Youn, J.K. and Park, S.
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                                                                                                                                                                                                                    Characterization and gene cloning of monoclonal antibody specific for the hepatitis B virus X protein Hybridoma 19 (1), 73-80 (2000)
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/product="immunoglobulin kappa light chain variable
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2 (bases 1 to 396)

Park, O.Y., Jin, Y.H., Lee, M., Kim, H.I., Youn, J.K. and Park, S. Direct Submission

Submitted (09-UNN-1999) Microbiology, Ajou Univ. School of Medicine, Paldalku, Suwon, Keyngkido 441-749, South Korea Location/Qualifiers
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90.8%; Score 359.4; DB 10; Length 396;
Best Local Similarity 94.7%; Pred. No. 6.9e-108;
Matches 372; Conservative 0; Mismatches 21; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                     1. 396
/organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="anti-HBx antibody"
                                                                                                   Mus musculus (house mouse)
Mus musculus
                                                                   AF157686.1 GI:5306067
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-07T-1992) Medina C. A., University of Texas Health Science Center at San Antonio, Microbiology, 7703 Floyd Curl Dr., San Antonio, TX, USA, 78284
Location/Qualifiers
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/citation=[1]
70. .408
/product="ig kappa light chain; Vk1-Jk2 region"
/citation=[1]
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MMIGKEAD 408 bp mRNA linear ROI
Mus musculus encoding immunoglobulin kappa light chain.
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/product="ig kappa light chain; Vkl exon"
/citation=[1]
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product="ig kappa light chain; Jk2 exon"
/citation=[1]
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immunoglobulin; immunoglobulin kappa light chain.
Mus musculus (house mouse)
Mus musculus
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/product="Vk1 region end/Jk2 start"
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Pred. No. 8.1e-108;
0; Mismatches 23;
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Search completed: September 26, 2005, 05:47:58 Job time: 2331 secs
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Series: IRAK Plate: 35 Row: f Column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                           BC031498 1008 bp mRNA linear ROD 13-FEB-2004 Mus musculus cDNA clone MGC:27817 IMAGE:3482714, complete cds.
300
                                                  253 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGAACAGATTTTACACTGAAAATC 312
                                                                                                        301 AGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT 360
                                                                                                                                            313 AGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTACTGCGTGCAAGGTACACATTTTCCG 372
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sheed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 1008)
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Submitted (06-J07-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                      361 CGGACGTTCGGTGGAGCCACCAAGCTGGAAATCAAA 396
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COMMENT
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TITLE

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/lab_host="DH10B"
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SQSLFYTMORMYLSWLIGPRGQPRFKLISLVSKLDSGVPDRFSGSGSGTDFFTLSISR
VEABDLGVYYCLQSTHFPYTPGGGTKLBINKADAAFTVSIRPPSSEQLTSGASVVCF
LNNFYPRDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="IGv; Region: Immunoglobulin domain variable region (v) subfamily"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="IGc; Region: Immunoglobulin domain constant region
subfamily"
/db_xref="CDD:cd00098"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 TCTGGAGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 AGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTACTGCTTGCAGAGTACACATTTTCCG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TATGTTGTGATGACCCAGACTCCACTCTCTTGTCGGTTACCATTGGACAACCAGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 GATGTTGTGATGACCCCAGACTCCACTTTGTCGGTTACCATTGGACAACCAGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAAAGACATATTTGAATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTTTATACTAATGGAAAAATGTATTTGAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 AGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 ATGATGAGTCCTGCCCAGTTCCTGTTTCTGCTAGTGCTCTCGATTCAGGAAATCAACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="Unknown (protein for MGC:27817)"
/protein_id="AAH11498.1"
/db_xref="GI:21594508"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 CGGACGTTCGGTGGAGCCACCAAGCTGGAAATCAAA 396
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                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
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                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="mix FVB/N, C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="CDD:cd00099"
418. .720
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(otqsu) Anola agog sidt

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

September 26, 2005, 05:09:16 ; Search time 86 Seconds
(without alignments)
593.632 Million cell updates/sec

US-10-010-942B-2

692 1 MMSPAQFLFLLVLWIRETNG......CWQGTHFPRTFGGGTKLEIK 132 Perfect score:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB 8 Maximum DB 8

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*

geneseqp1980s:* geneseqp1990s:* Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2000s:* geneseqp2001s:* 8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Mouse 3D6	Murine 3D	Chimeric	Mouse bin	Anti-Stre	Humanised	Light (ka	Antibody	Light cha	Humanised	Humanised	Mouse MAb	Mouse ant	Humanised	Humanised	Sequence	Murine an	Mouse imm	Sequence	Rat Prote	Heterorec	Murine PS	Heterorec	Chimeric	
	ion	Mou		S	Mod		_		Art	Lig	_	•	Mou		_	Hum	Sed	_		-	Rat	_	Mur	Het	_	
	Description	Abg76923	Adr88406	Adm72033	Adp45549	Abb79729	Abp58274	Aar12361	Ado00819	Ado43845	Abg76925	Adr88409	Aar12239	Abg74244	Abg76931	Adr88415	Aar24712	Aae07032	Adq89324	Aar24811	Add47025	Adq76076	Aae03751	Adq76088	Aae03756	
SUMMAKIES		3	9	3	6	6	4	1	o	S.	r.	6	6	4	-	5	7	7	4	н	S	9	н	8	9	
NIMIN S	ΩI	ABG76923	ADR88406	ADM7203	ADP45549	ABB7972	ABP58274	AAR12361	AD000819	AD043845	ABG76925	ADR88409	AAR12239	ABG74244	ABG76931	ADR88415	AAR24712	AAE07032	ADQ89324	AAR24811	ADD47025	ADQ76076	AAE03751	ADQ76088	AAE03756	
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	Length	132	132	238	238	135	239	132	133	133	132	132	131	132	132	132	132	142	142	239	239	113	113	113	218	
de	Query Match	100.0	100.0	94.7	94.4	93.9	93.1	95.6	95.6	95.6	92.5	92.5	92.3	91.9	91.0	91.0	90.8	87.6	87.6	86.0	85.1	82.8	82.5	82.5	82.5	
	Score	692	692	655	653	650	644	641	641	641	640	640	639	636	630	630	628	909	909	595	589	573	571	571	571	
	Result No.	-	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	

Adq76082 Heterorec Adq76086 Heterorec Adq76080 Heterorec Adq76080 Heterorec Adq76080 Heterorec Adq25828 Anti-CD30 Adq76090 Heterorec Adq76090 Heterorec Adq76074 Heterorec Adq76074 Heterorec Adq76084 Mutine 1D Aau09918 Murine mA Abg75527 Mouse mAb Adf98231 Murine mA	Abr61865 Mouse MAb Adq31246 Murine 1A Adq89231 Mouse imm Adj95990 Immunoglo Adj95992 Immunoglo
ADQ76082 ADQ76096 ADQ76094 ADQ76092 ADQ52828 ADG25828 ADQ76090 ADQ76094 AAQ62533 AAE06946 AAR06918 AAE06998	ABR61865 ADQ31246 ADQ89231 ADJ95990 ADJ95992
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	41 42 44 45

ALIGNMENTS

ABG76923 standard; protein; 132 AA RESULT 1 ABG76923

(first entry)

05-NOV-2002

Mouse 3D6 VL protein.

Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC; variable region complementarity determining region; 3D6; 10D5; variable framework region; amyloidogenic disease; Alzheimer's disease; amyloid deposit; variable light chain; VL; variable heavy Chain; VH; nootropic; neuroprotective; inhibitor of beta amyloid accumulation; Abeta.

Mus musculus.

WO200246237-A2.

13-JUN-2002.

06-DEC-2001; 2001WO-US046587.

06-DEC-2000; 2000US-0251892P.

(NEUR-) NEURALAB LTD. (AMHP) WYETH.

WPI; 2002-519658/55.

Basi G, Saldanha J,

Ë

Yednock

N-PSDB; ABS59426

Novel light/heavy chain of humanized immunoglobulin for treating amyloidogenic disease, has 3D6/10D5 variable region complementarity determining regions and variable framework region from human acceptor immunoglobulin.

Claim 67; Fig 1; 171pp; English.

The present invention relates to new humanized immunoglobulin (Ig) light chain (LC) or heavy chain (HC) comprising variable region complementarity determining regions from 3D6/10D5 Ig LC or HC variable region sequence, and variable framework region from human acceptor Ig LC or HC sequence. The invention is useful for preventing or treating an amyloidogenic disease or Alzheimer's disease in a patient. The invention is also useful

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amyloid deposits in a patient. The present amino acid a mouse 3D6/10D5 variable light (VL) chain or chain protein of the invention
                                                                                                                                                                                                                                                                                                                                   LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                         61 LLQRPGQSPKRLIXLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3D6; light chain variable region; immunoglobulin; complementarity determining region; CDR; 10D5; variable framework region; neuroprotective; nootropic; gene therapy; amyloidogenic disease;
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                                                                                                                                             Length 132;
                                                                                                                                                                                        Indels
                                                                                                                                        100.0%; Score 692; DB 5;
100.0%; Pred. No. 6.3e-55;
ive 0; Mismatches 0;
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/label= signal peptide
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/label= mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 2; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR88406 standard; protein; 132 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2004; 2004WO-US007503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-2003; 2003US-00388389
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                                                                                                                                                                                                                                                                                                                                                                                                                             RIFGGGIKLEIK 132
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Best Local Similarity 100.
Matches 132, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NEUR-) NEURALAB LTD
for in vivo imaging
sequence represents
variable heavy (VH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's disease
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                                                                                              Sequence 132 AA;
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ADRIBATOR ADR
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The invention relates to a novel humanised immunoglobulin light or heavy chain. The humanised immunoglobulin light or heavy chain comprises: variable region complementarity determining regions (CDR's) from the 3D6 immunoglobulin light chain variable regions equence of 132 amino acids fully defined in the specification (ADR88406), or heavy chain variable

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region sequence of 138 amino acids fully defined in the specification sequence of 138 amino acids fully defined in the specification (ADR88408); or from the 10D5 immunoglobulin light chain variable region sequence of 131 amino acids given in the specification (ADR88418) or havy chain variable region sequence of 142 amino acids fully defined in the specification (ADR88420); and a variable framework region from a common immunoglobulin light or heavy chain sequence, provided that at least one framework residue is substituted with the corresponding amino acid residue from the mouse 3D6 or 10D5 light or heavy chain corresponding an incorrective residue is a residue that non-covalently binds antigen directly, a residue is a residue that concovalently binds antigen directly, a residue is a residue that concovalently binds antigen directly, a residue directly, a collective and nootropic activity, and may have a use in gene therapy. The composition and methods are useful for preventing or treating an amyloidogenic disease, such as Alzheimer's disease. The variable region sequence is useful in producing a three-dimensional image of a 3D6 or 10D5 immunoglobulin immunoglobulin immunoglobulin light chain variable region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-GPC3 antibody; cell disruption; anti-cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody against the N terminus of glypican 3(GPC3) causes cell disruption and is useful as an anticancer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 692; DB 8; Length 132; 100.0%; Pred. No. 6.3e-55; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ito Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohizumi I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric mouse-human antibody M3C11 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aburatani H, Midorikawa Y, Nakano K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADM72033 standard; protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-SEP-2003; 2003WO-JP011318.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 RTFGGGTKLEIK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-269573/25.
N-PSDB; ADM72032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPC3; glypican 3;
cytostatic; M3C11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004022739-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM72033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
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useful

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Gaps

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Score 653; DB 8; Length 238; Pred. No. 4.2e-51; 6; Mismatches 2; Indels

94.4%;

9

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61 LQRPGQSPKRLIYLVSKLDSGVPDRPTGSGSGTDFTLKISRVEAEDLGLYYCWQCTHFPQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
associated with nerve repair. The binding molecule has neuroprotective activity, and can be used in gene therapy. The binding molecule is useful in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence represents a mouse binding molecule 1107 light chain, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSPAQFLFLLVLWIRETSGDVLLTQTPLTLSITIGQPASISCKSSQSLLHSDGKTYLNWL
                                                                                                                                                                                                                                                                                                                                                                                    2 MSPAQFLFLLVLWIRETNGYVVWTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWL
                                                                                                                                                                                                                                                                                                                              Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 TFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                            Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002068066-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WIMS L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB79729;
                                                                                                                                                                                                                                                                     Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TRIN/)
(WIMS/)
(CHEN/)
(ANDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SHIW/)
(MORR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shi W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB79729
            8888888
                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LQRPGQSPKRLIYLVSKLDSGAPDRFTGSGSGTDFTLKISRVEAEDLGIYYCMQGTHFPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nogoà polypeptide, human NiG, human NiG-DZO or human NogoA 623-640 with a dissociation constant of less than 1000nM. Also described: (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the expression system; (4) a pharmaceutical composition comprising the binding molecule and a carrier or diluent; and (5) treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
                                                               The invention relates to an antibody against the N terminus of glypican 3 (GPC3). The antibody can be used for causing cell disruption and can be uses as an anti-cancer agent. The present sequence represents a chimeric mouse-human antibody M3C11 light chain.
                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-
D20 or NogoA623-640, useful in preparing a composition for treating CNS
injury or neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a binding molecule which binds to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWL
                                                                                                                                                                                                                                                                                                                                                                                    2 MSPAQFLFLLVLWIRETNGYVVWHTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWL
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vitaliti A;
                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                               94.7%; Score 655; DB 8; Length 238; 94.7%; Pred. No. 2.8e-51; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schwab ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse binding molecule 11C7 light chain SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schnell L,
         Example 4; SEQ ID NO 18; 122pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; SEQ ID NO 3; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADP45549 standard; protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oertle T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-DEC-2003; 2003WO-EP013960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS PHARMA GMBH.
(UYZU-) UNIV ZUERICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-2002; 2002GB-00028832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-SEP-2004 (first entry)
                                                                                                                                                                                                                                                                                                                           Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 TFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFGAGTKLELK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-468818/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mir AK,
                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                            Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004052932-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mouse; antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUN-2004.
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Zurini M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP45549;
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP45549

IID ADP4

XX ADP4

XX ADP4

XX ADP4

XX ADP4

XX ADP5

XX ADP6

X
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         83666688
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Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody; anticaries; transgenic plant; transgenic animal; caries;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the protein sequence of the light chain variable region (VL) of the murine monoclonal antibody SWLA3 (1gG), which binds specifically to the surface antigens of cariogenic type c Streptococcus mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC HB 12558) hybridoma cells. In an example from the invention, chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           particular
purified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment and prevention of dental caries in mammals, in particular humans by orally administering genetically engineered or purified antibodies that bind to surface antigens of carcinogenic organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson MH;
                                                                                                                                                      Anti-Streptococcus mutans surface antigen MAb SWLA3 VL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wims
                                                                      ABB79729 standard; protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Fig 3A; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trinh K,
                                                                                                                                                                                                                                                                                                                       15-JUN-2001; 2001US-00881823.
                                                                                                                                                                                                                                                                                                                                                  99US-00378577
                                                                                                                           (first entry)
121 TFGGGTKLEIK 131
                                                                                                                                                                                                             immunotherapy; therapy.
                                                                                                                                                                                                                                                                                                                                                                                          S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ANDERSON M H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morrison SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-565838/60.
                                                                                                                                                                                                                                                                                                                                                                            SHI W.
MORRISON 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABN84610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           humans by orally
                                                                                                                                                                                                                                                                                                                                                                                                       TRINH K.
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WPI; 2003-183835/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR12361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                and human antibody constant regions. Such chimeric monoclonal antibodies can be used to prevent or treat dental caries in humans. The antibodies engage the effector apparatus of the human immune system when they bind cariogenic organisms, resulting in their destruction. The chimeric antibodies may be produced in edible plants, in transgenic animals, or in chicken eggs for oral ingestion
                                                                                                                                                                                                                                                                                                                                                61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                                      61 LLQRPGQSFKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "light chain variable region, claimed in Claim 4"
  monoclonal antibody TEFE was produced comprising SWLA3 variable regions
                                                                                                                                                                                                                                                                                              1 MMSPAQPLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21. .239
/label= Mature_peptide
/note= "the mature light chain is claimed in Claim 5"
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                 ;
                                                                                                                                                                                           Score 650; DB 5; Length 135; Pred. No. 4.2e-51;
                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .20
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP58274 standard; protein; 239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised 3D6 antibody light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "CDR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "CDR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114. .122
/note= "CDR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-2002; 2002WO-US011853
                                                                                                                                                                                           Query Match
Best Local Similarity 93.2%;
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| ||||||
|121 LTFGAGTKLELK 132
                                                                                                                                                                                                                                                                                                                                                                                                                               121 RTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsurushita N, Vasquez M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44. .59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ELIL ) LILLY & CO ELI
                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                         Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200288306-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP58274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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ARBFS 8274
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The present sequence is that of a preferred light chain of a humanised antibody of the present invention. In the variable region of this sequence, the complementarity determining regions (CDRs) originate from sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 3D6 and the framework region from human germline Vk segment DPK19 and J segment JK4. Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 3D6 antibody. The invention includes antibodies, single chain antibodies, and their cragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
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                                                                   New humanized forms of mouse 3D6 antibodies, useful for treating Down's syndrone, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, or for inhibiting formation of or reducing Abeta plaque in the brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MMSPAQFLFLLVLWIRETNGDVVMTQSPLSLPVTLGQPASISCKSSQSLLDSDGKTYLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric antibodies; immunoconjugates; HIV; AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 644; DB 6;
Pred. No. 2.8e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
                                                                                                                                                                                                                                                                       Disclosure; Page 12-13; 54pp; English.
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90.9%;
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N-PSDB; ABZ24632, ABZ24634.
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Matches 120; Conservative
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                                                                                         This is the light (kappa) - chain variable (V) region of a mouse monoclonal antibody (MAb), 4D12, and is specific for an HIV-1 viral haritgen. It is used in the construction of a chimeric MAb comprising heavy and light chains having murine V regions and human C regions. The chimeric MAbs are more effective than murine MAb 4D12 since they have an increased compatibility in humans. The heavy and light chain V-regions are joined by manipulating their respective joining (J) regions, to generate restriction enzyme recognition sites. The chimeric MAbs can be used as immunoconjugates, in association with e.g. toxins for HIV treatment. They can also be used in diagnosis of HIV. See also AAQ12056-62. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct DR field.)
                                                                                                                                                                                                                                                                                                                                            61 LLQRPGQSPKRLIYLVSKLDSGVPDRPTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                       61 FLQRPGQSPKRLLYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGSHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11; beta-amyloid-related disease; Alzheimer's disease; Abeta sectrease; cleavage site; immunogen; murine; antibody; light chain; variable region; JRF/cAbeta40/10.
                                         New chimeric mouse-human antibodies - used to detect, kill and remove HIV -1 antigen from sample.
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                                                                                                                                                                                                                                                                                                               1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                        92.6%; Score 641; DB 2; Length 132; 90.9%; Pred. No. 2.7e-50; ive 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                        Disclosure; Fig 18; 107pp; English
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/note= "CDR1"
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/note= "CDR2"
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                                                                                                                                                                                                                                                                                                                                                                                       121 RTFGGGTKLEIK 132
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                                                                                                                                                                                                                                                                   Best Local Similarity 90.9
Matches 120; Conservative
           WPI; 1991-178105/24.
                    N-PSDB; AAQ12063
                                                                                                                                                                                                                                     Sequence 132 AA;
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The present invention relates to an antibody expressed by the hybridoma cells JEJPRD/hAbetall/1 and JEJPRD/hAbetall/2, which is capable of cells JEJPRD/hAbetall/1 and JEJPRD/hAbetall/2, which is capable of specifically recognizing human Amyloid-beta 11 N-terminal site (i.e., Abetall-x peptides). The antibody is useful for diagnosing beta-amyloid-response to therapy of Alzheimer's disease and other beta-amyloid related diseases and in passive immunization as a method for treating such diseases. A humanized form of the antibody is useful for manufacturing a medicament for treating, preventing or reversing cognitive decline in clinical or pre-clinical Alzheimer's Disease, Down's syndrome, Hereditary Cerebral Hemorrhage with Amyloidosis of the Dutch-Type, cerebral amyloid manipulation of amyloid plaques or the effects of toxic soluble Amyloid-beta sepecies in humans. It can also be used in assay systems such as
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                                                                                                                                                                                                              New N-11 truncated amyloid-beta monoclonal antibodies specific for human Amyloid-beta 11 N-terminal site (A-betall-x peptides), useful for diagnosing or treating beta-amyloid-related diseases e.g. Alzheimer's
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                                                                        Mercken MH, Vandermeeren MMPP;
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/note= "CDR2"
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Matches 121; Conservative
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(JANC ) JANSSEN PHARM NV
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The present invention relates to new humanized immunoglobulin (Ig) light chain (LC) or heavy chain (HC) comprising variable region complementarity determining regions from 3D6/10D5 Ig LC or HC variable region sequence, and variable framework region from human acceptor Ig LC or HC sequence. The invention is useful for preventing or treating an amyloidogenic disease or Alzheimer's disease in a patient. The invention is also useful for in vivo imaging amyloid deposits in a patient. The present amino acid sequence represents a humanized 3D6 variable light (VL) chain or variable heavy (VH) chain protein of the invention
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Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC; variable region complementarity determining region; 3D6; 10D5; variable framework region; amyloidogenic disease; Alzheimer's disease; amyloid deposit; variable light chain; VL; variable heavy chain; VH; nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
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90.2%; Pred. No. 3.3e-50;
.ive 10; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                          06-DEC-2001; 2001WO-US046587.
                                                                                                                                                                                                                                                                                                                             06-DEC-2000; 2000US-0251892P.
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Best Local Similarity 90.2'
Matches 119; Conservative
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121 RTFGQGTKVEIK
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                                                                                                                                                                                                                                                                                                                                                                  (NEUR-) NEURALAB LTD
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                                                                                                                                                           musculus.
                                                                                                                                      Homo sapiens
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                                                                                                                                                                             Synthetic.
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ADR88409
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a monoclonal antibody which specifically recognizes human Amyloid-betail-x peptides. These peptides result from overexpression of BACE-1 which causes additional cleavage at the +11 site of amyloid-beta, generating shorter fragments known as Amyloid-betail-x peptides. BACE-1 is the major beta-secretase required for cleavage of peta-amyloid precursor protein. The antibody is useful for detecting the presence of amyloid-beta peptides in a tissue or fluid sample and for diagnosing beta-amyloid-related diseases. It is particularly useful for prognosing and monitoring response to therapy of Alzheimer's disease and other beta-amyloid related diseases and in passive immunization as a method for treating such diseases. A humanized form of the antibody is useful for manufacturing a medicament for treating, preventing or reversing cognitive deciline in clinical or pre-clinical Alzheimer's Disease, Down's syndrome, Hereditary Cerebral Haemorrhage with Amyloidasis of the Dutch-Type, cerebral amyloid angipathy or other beta-amyloid-related diseases, or to inhibit the formation of amyloid related diseases, or to inhibit the formation of amyloid-betall-to.

The effects of toxic soluble Amyloid-beta species in humans. The present sequence represents the light chain variable region of an anyloid-betall-to.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LLQRPGQSPKRLIYLVSKLDSGVPDRFSGSGSGTDFTLKINRVEAEDLGVYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                           New N-11 truncated amyloid-beta monoclonal antibodies specific for human Amyloid-beta 11-x peptides (A-beta11-x peptides), useful for diagnosing or treating beta-amyloid-related diseases e.g., Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.6%; Score 641; DB 8; Length 133; 91.7%; Pred. No. 2.7e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised 3D6 light chain variable region #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 38-39; 50pp; English
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                                                                                                                                                                                                                                                     Mercken MH, Vandermeeren MMPP,
                           /note= "CDR3"
                                                                                                                                        09-SEP-2003; 2003WO-EP010092
                                                                                                                                                                             27-SEP-2002, 2002WO-EP011062
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                                                                                                                                                                                                                (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                          WPI; 2004-316181/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 133 AA;
                                                              WO2004029630-A1
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                                                                                                   08-APR-2004
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Gaps

9 9 120

121 RTFGQGTKVEIK 132

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The invention relates to a novel humanised immunoglobulin light or heavy chain. The humanised immunoglobulin light or heavy chain comprises:

"A variable region complementarity determining regions (CDR's) from the 3D6 immunoglobulin light chain variable region sequence of 132 amino acids fully defined in the specification (ADR88408), or heavy chain variable region acquence of 131 amino acids fully defined in the specification (ADR88418) or feary chain variable region sequence of 131 amino acids given in the specification (ADR88418) or heavy chain variable region sequence of 142 amino acids fully defined in the specification (ADR88418) or human acceptor immunoglobulin light or heavy chain sequence, provided that at least one framework residue is substituted with the corresponding anino acid residue from the mouse 3D6 or 10D5 light or heavy chain corresponding variable region sequence, where the framework residue that con-covalently binds antigen directly, a residue adjacent to a CDR, a CDR interacting residue or a residue participating in the VL-VH interface.

"A nantibody of the invention has neuroprofective and noctropic activity, and may have a use in gene therapy. The composition and methods are useful for preventing or treating an amyloidogenic disease, such as three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin chain, or its domain. The present sequence represents a humanised immunoglobulin of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized antibodies that recognize beta amyloid peptides, useful for preventing or treating amyloidogenic diseases, such as Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complementarity determining region; CDR; 10D5; variable framework region; neuroprotective; nootropic; gene therapy; amyloidogenic disease; Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MMSPAQFLFLLVLWIRETNGYVWMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
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                                                                                                                                   1. .20
/label= signal peptide
21. .132
/label= mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 54; SEQ ID NO 5; 176pp; English.
                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         Yednock T;
                                                                                                                                                                                                                                                                                                       12-MAR-2004; 2004WO-US007503.
                                                                                                                                                                                                                                                                                                                                             12-MAR-2003; 2003US-00388389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                         Saldanha JW,
                                                                                                                                                                                                                                                                                                                                                                                  (NEUR-) NEURALAB LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-668880/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 132 AA;
                                                                                                                                                                                                                             WO2004080419-A2
                                                                                                                                                                                                                                                                                                                                                                                                   (AMHP ) WYETH
                                                                                                                                                                                                                                                                    23-SEP-2004
                                                                            Synthetic
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                                                                                                                                 Peptide
                                                                                                                                                                      Protein
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The mouse VL gene product may be used to produce chimeric mouse- human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LLQRPGQSPKRLIYLVSKLDSGVPDRPTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FLQRPGQSPKRLLYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYCWQGSHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                             New chimeric mouse human antibodies - used in treatment, diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASFSCKSSQSLLDSDGKTFLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
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                                                                                                                                                                                                                                                                                                                                                                       Ghoshdasti P, Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 18; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG74244 standard; protein; 132 AA.
          AAR12239 standard; protein; 131 AA.
                                                                                                           Mouse MAb 4D12 L chain V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          prophylaxis of HIV infections.
                                                                                                                                                                                                                                                        89US-00433703.
                                                                 (revised)
(first entry)
                                                                                                                                                                                                                                                                                                              (XOMA ) XOMA CORP.
(GREC ) GREEN CROSS CORP.
(ZOMA-) ZOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        Setter MD, Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-178106/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ12019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 131 AA;
                                                                                                                                       HIV-1; chimera
                                                                                                                                                                                                                                                                                   13-NOV-1989;
                                                                 25-MAR-2003
19-AUG-1991
                                                                                                                                                                                                                                                        13-NOV-1989;
                                                                                                                                                                                                WO9107494-A.
                                                                                                                                                                                                                            30-MAY-1991
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                                      AAR12239;
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ABG74244
ID ABG74
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AC ABG74
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DT 22-AP
AAR1223
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(first entry)

22-APR-2003

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a chimaeric molecule comprising the GD3

(ganglioside antigen) binding domain of antibody MB3.6, with any of 3

variable gene sequences, or the PSMA (protate-specific membrane antigen)

binding domain of antibody 3D8, 4D4 and 3B11, with variable gene

sequences, the zeta signalling chain of the T cell receptor and an

intervening CD8alpha hinge in which cysteine residues have been mutated.

The chimaeric molecules expressed in T cells or NK cells or other

effector cells are useful in treating patients with cancers expressing

the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3B11 derivatives),

and/or together with each other or with heterologous constructs to engage

additional stimulatory and functional properties of the effector cells to

enhance the antitumour therapeutic efficacy (claimed). They are

changed the settle in disorders including melanoma, neuroendocrine

tumours and prostate and small cell lung cancer. The present sequence

represents the mouse antibody 3D8 light chain variable region
                                     T-cell receptor; cytostatic; dermatological; neuroprotective; immunostimulant; GD3; ganglioside antigen; MB3 6; PSWA; tumour; 3D8; 4D4; SIII; prostate-specific membrane antigen; zeta signalling chain; CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer; light chain variable region; mouse.
                                                                                                                                                                                                                                                                                                                                                                                 aB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGTHFPH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSPAQFLFLLVLWIQETNGDVVWTQTPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWL 60
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                                                                                                                                                                                                                                                                                                                                                                           New chimeric molecule useful in treating patients with disorders, such a melanoma, neuroendocrine disorders, prostate and small cell lung cancer comprises GD3 and/or PSMA binding domains of antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 MSPAQFLFLLVLWIRETNGYVVWTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWL
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Pred. No. 7.6e-50;
4; Mismatches 4; Indels
           Mouse antibody 3D8 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 13; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.9%;
                                                                                                                                                                                                          10-DEC-2001; 2001US-00006773
                                                                                                                                                                                                                                      30-NOV-2000; 2000US-0250087P, 30-NOV-2000; 2000US-0250089P,
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                                                                                                                                                                                                                                                                               (JUNG/) JUNGHANS R P.
                                                                                                                                                                                                                                                                                                                                     WPI; 2003-208946/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Tocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 132 AA;
                                                                                                                                                      US2002132983-A1
                                                                                                                                                                                                                                                                                                           Junghans RP;
                                                                                                                                                                                  19-SEP-2002
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ABG76931 standard; protein; 132 AA.

RESULT 14
ABG76931
ID ABG76
XX
AC ABG76

ABG76931;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLORPGOSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LLQKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCWQGTHFP 120
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                                                                                                  Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC; variable region complementarity determining region; 3D6; 10D5; variable framework region; amyloidogenic disease; Alzheimer's disease; amyloid deposit; variable light chain; VL; variable heavy chain; VH; nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel light/heavy chain of humanized immunoglobulin for treating amyloidogenic disease, has 3D6/10D5 variable region complementarity determining regions and variable framework region from human acceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
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89.4%; Pred. No. 2.7e-49;
live 10; Mismatches 4.
                                                    Humanised 3D6 light chain variable region #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 55; Page 157; 171pp; English.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NEUR-) NEURALAB LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-519658/55.
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Synthetic.
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05-NOV-2002
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                                                                                                                                                                                                                                                         Abeta.
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16-DEC-2004 (first entry) Synthetic

Humanised 3D6 immunoglobulin light chain variable region SEQ ID NO:11.

3D6; light chain variable region; immunoglobulin; complementarity determining region; CDR; 10D5; variable framework region; neuroprotective; nootropic; gene therapy; amyloidogenic disease; Alzheimer's disease.

1. .20 /label= signal peptide 21. .132 /label= mature protein Location/Qualifiers Key Peptide Protein

WO2004080419-A2.

23-SEP-2004

12-MAR-2004; 2004WO-US007503.

12-MAR-2003; 2003US-00388389.

(NEUR-) NEURALAB LTD. (AMHP) WYETH.

Yednock T; Saldanha JW, Ваві G,

WPI; 2004-668880/65.

New humanized antibodies that recognize beta amyloid peptides, useful for preventing or treating amyloidogenic diseases, such as Alzheimer's disease

Claim 55; SEQ ID NO 11; 176pp; English.

The invention relates to a novel humanised immunoglobulin light or heavy chain. The humanised immunoglobulin light or heavy chain comprises:

variable region complementarity determining regions (CDR's) from the 3D6 immunoglobulin light chain variable region sequence of 132 amino acids fully defined in the specification (ADR88406), or heavy chain variable region sequence of 138 amino acids fully defined in the specification (ADR88408), or from the 10D5 immunoglobulin light chain variable region sequence of 131 amino acids given in the specification (ADR88418) or heavy chain variable region sequence of 142 amino acids fully defined in the specification (ADR88418) or human acceptor immunoglobulin light or heavy chain sequence, provided that at least one framework residue is substituted with the corresponding amino acid residue from the mouse 3D6 or 10D5 light or heavy chain variable region sequence, where the framework residue that con-covalently binds antigen directly, a residue as residue that con-covalently binds antigen directly, a residue adjacent to a CDR interacting residue or a residue participating in the VL-VH interface.

An antibody of the invention has neuroprofective and noctropic activity, and may have a use in gene therapy. The composition and methods are useful for preventing or treating an amyloidogenic disease, such as Alzhaimmer's disease. The variable region sequence is useful in producing a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin of the invention.

Sequence 132 AA;

; 0 91.0%; Score 630; DB 8; Length 132; 89.4%; Pred. No. 2.7e-49; ive 10; Mismatches 4; Indels Best Local Similarity 89.44 Matches 118; Conservative Query Match

1 MMSPAQFLFLLVLWIRETNGDVVWTQSPLSLPVTPGEPASISCKSSQSLLDSDGKTYLNW 60 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW

> a 8

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61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120

61 LLQKPGQSPQRLIYLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYXCWQGTHFP 120 121 RTFGGGTKLEIK 132 |||| |||:||| 121 RTFGQGTKVEIK 132 ð

completed: September 26, 2005, 07:16:20 ne : 89 secs Search co

(otqsu) Anola 9009 sinj

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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- protein search, using sw model OM protein September 26, 2005, 06:27:34; Search time 25 Seconds (without alignments) 508.025 Million cell updates/sec Run on:

US-10-010-942B-2

692 1 MMSPAQFLFLLVLWIRETNG......CWQGTHFPRTFGGGTKLEIK 132 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	a kappa	kappa chain	Ig kappa chain V r	proteolytic antibo		Ig kappa chain V r	Ig kappa chain V r	HUNVK protein prec	Ig kappa chain V r	kappa	g kappa chain	g kappa	g kappa	kappa chain	g kappa chain	Б	ס		g kappa	ρ	kappa	g light chain	g kappa	Б	kappa chain	b	kappa chain pr	g kappa chain	מ
SUMMARIES	Ω	C32513	831577	F30560	A55491	A36259	820709	PL0273	S42611	A33730	823230	S22902	S40324	K2HURP	S22658	A24452	S40322	PH1055	S42186	S42268	S42267	S09259	PH1056	840312	D29380	S40355	S26882	S49572	S40374	B49002
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	eng	132	131	113	112	112	111	112	133	101	133	142	133	133	140	133	132	103	91	120	120	131	103	126	131	131	132	114	118	114
	Query Match	98.0	4	н	80.1	9	79.0	~	74.6	74.4	74.4	74.1	74.0	73.4	72.6	71.7	71.0	70.1	68.8		68.4	67.9	67.3	6.99	6.99	66.8	8.99	66.7	66.5	66.3
	Scor	678	587	266	554	548	547	536	216	515	515	513	512	508	502.5	496	491	485	476	473	473	470	466	463	463	462.5	462	461.5	9	458.5
	Result No.	-	8	e	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	70	21	22	23	24	25	26	27	28	29

Ig kappa chain pre	Ig kappa chain V-J	Ig kappa chain V r	Ig light chain pre	anti-digoxin trans	Ig kappa chain pre	Ig kappa chain - h	Ig kappa chain pre	Ig kappa chain pre	Ig kappa chain pre	Ig kappa chain - h	Ig kappa chain pre	Ig kappa chain V r			
B34904	S40357	A31807	B39276	PH0106	C34904	S40376	S40338	S40373	840321	D34904	B30577	G34903	S40342	B32513	838715
7	~	~	7	~	7	7	7	~	7	7	~	~	7	~	0
131	136	112	131	132	131	134	122	128	130	131	131	131	135	131	115
66.2	66.2	62.9	62.9	65.8	65.6	65.4	65.3	65.2	65.1	65.0	65.0	64.7	64.7	64.6	64.5
			9	'n	4	'n	22	121	5.5	150	150	48	48	147	46
458	458	456	45	45	4	452	4	4	45(•	•	4	4	4	4

ALIGNMENTS

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Grappa chain precursor V region (BXW14) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus-1842-1910 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Accession: C32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; I.J.; Cin. Invest. 82, 82-860, 1988
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and janglerence number: A94689; MulD:88331394; PMID:3138286
A;Accession: C32513
A;Reference number: A94689; MulD:89331394; PMID:3138286
A;Accession: C32513
A;Residues: 1-132 <KOF>
A;Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940
C;Superfanily: immunoglobulin V region; immunoglobulin homology
C;Superfanily: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 Kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: S31577
R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.
R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.
R;Recinos: Marsil Data Library, January 1993
A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for two antic A;Reference number: S31577
A;Accession: S31577
A;Accession: S31577
A;Accession: S31577
A;Accession: S31577
A;Residues: 1-131 <-REC>
A;Cross-references: EMBL: Z19575; NID:g53983; PIDN:CAA79627.1; PID:g53984
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 98.0%; Score 678; DB 2; Length 13 Best Local Similarity 97.7%; Pred. No. 1.6e-51; Matches 129; Conservative 2; Mismatches 1; Indels
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셤 ò 유 ò 셤

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Gypecies: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S20709
R;Brennand, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osbc submitted to the EMBL Data Library, April 1992
A;Description: Binding specificity and variable region sequences of two monoclonal antibc A;Reference number: S20706
A;Reference number: S20709
A;Reference type: DNA
A;Residues: 1-111 <BRE>
A;Cross-references: EMBL:Z11917; NID:952655; PIDN:CAA77975.1; PID:952656
C;Superfeanily: immunoglobulin V region; immunoglobulin homology
C;Superfeanily: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: GB:M30458; GB:M30459; GB:M30480; GB:M30481; GB:M30482; GB:M30483 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin homology File-95/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                     ig kappa chain V region (TE34) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Bate: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 21-Jan-2000
C;Bate: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 21-Jan-2000
C;Accession: A36259
R;Zilber, B.; Scherf, T.; Levitt, M.; Anglister, J.
B;ochemistry 29, 10032-10041, 1990
A;Title: NRR-derived model for a peptide-antibody complex.
A;Reference number: A36259
A;Accession: A36259
A;Acturus: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 < ZIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 VVMIQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS
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                                                                                       2 VVMTQTPLTISVTIGQPASISCKSSQSLLHTDGKTYLIMLLQRPGQSPKRLIYLVSKLDS
                                                        22 VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS
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   0; Gaps
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   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.2%; Score 548; DB 2; ilarity 94.6%; Pred. No. 2.1e-40; Conservative 2; Mismatches 4.
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Pred. No. 2.5e-40;
6; Mismatches 2
4; Mismatches
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Best Local Similarity 92.7%;
Matches 102; Conservative
   105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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Matches
   Matches
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F30560
Ig Aspa chain V region (28.4.10A) - mouse (fragment)
Ig Kappa chain V region (28.4.10A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Date: 73-Mar-1980 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
R;Accession: R30560
R;Mateuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclo
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C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55491
S;Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, J. Biol. Chem. 269, 32389-32393, 1994
A;Title: Molecular cloning of a proteolytic antibody light chain.
A;Reference number: A55491; MUID:95096089; PMID:7798238
A;Accession: A55491
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                                                                                                                                                                                                                                                                                                       LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
                                                                                                                                                                                                                   1 MSPAQPLFLVVLSIQEINGDVVMTQAPLTLSVTLGQPASISCKSSHSLLSIDGKTYLNWL 60
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                                                                                                                                                                                    MSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
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Pred. No. 6e-42;
2; Mismatches 2; Indels
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                                                                 Length 131;
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-112 < GGAO-
A;Cross-references: UNIPROT: Q8K0F8; GB:L34775
A;Note: authors translated the codon TAT for residue 37 as Thr
A;Note: authors translated the codon TAT for residue 37 as Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology < IMM>
                                                                                                                      10; Indels
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                                                              84.8%; Score 587; DB 2; ilarity 86.3%; Pred. No. 1.1e-43; Conservative 8; Mismatches 10;
   F;35-114/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 96.4%;
Matches 107; Conservative
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Best Local Similarity
                                                              Query Match
Best Local Similarity
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A, Status: preliminary
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A;Residues: 1-101 <LAW>
A;Cross-references: GB:M25996; NID:g197109; PIDN:AAA38911.1; PID:g197110
A;Cross-references: GB:M25996; NID:g197109; PIDN:AAA38911.1; PID:g197110
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                      C;Accession: A33730
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Barly rearrangements of genee encoding murine immunoglobulin kappa-chains, unli}
A;Reference number: A33730; MUID:89367325; PMID:2505260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S23230

Ig kappa chain precursor V-J region - human (fragment)

C;Species: Homo mapiens (man)

C;Species: Homo mapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C;Accession: S23230

R;Kennedy, M.A.

A;Title: Movel Chromosome translocation caused by fusion of immunoglobulin heavy and lightherence number: S23230; MUID:91178438; PMID:1840606
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  Ig kappa chain V region (1.60) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS
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A;Molecule type: DNA
A;Rebidues: 1-133 <KEN>
A;Crose-references: EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:g34000
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 101;
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Pred. No. 1.3e-37;
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42611
R;Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.
J. Neuroimmunol. 36, 29-39, 1992
A;Title: DNA sequence analysis and comparison of the variable heavy and light chain regi
Ig Kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: PLO273
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A. Kaphomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A. A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic A;Reference number: PLO231; MUID:90111618; PMID:2104919
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Pred. No. 2.3e-39;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-112 <SHL>
A;Cross-references: UNIPROT: Q8KOF8
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-55/Domain: immunoglobulin homology <IMM>
F;24-39/Region: cmplementarity-determining 1
F;40-54/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;94-102/Region: complementarity-determining 3 F;103-112/Region: framework 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;55-61/Region: complementarity-determining 2 P;62-93/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.5%;
93.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUNVK protein precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 93.7
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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121 LTFGGGTKVEI 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-133 <SPA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S42611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-133/Froduct: Ig kappa chain V-II region (RPMI) #status predicted <MMT>
F;21-43/Region: framework 1
F;36-115/Domain: immunoglobulin homology <IMM>
                   C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A01890
R;Klobeck, H.G; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A;Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A;Accession: A01890
                                                                                                                                                                                                                                   A;Wolecule type: DNA
A;Residues: 1-133 «KLO»
A;Residues: U1-133 «KLO»
A;Residues: UNIPROT:P06310
A;Note: the sequence was determined from the differentiated gene
g kappa chain precursor V-II region (RPMI) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;44-59/Region: complementarity-determining 1 F;60-74/Region: framework 2
                                                                                                                                                                                                                                                                                                                                                                    A,Gene: GDB:IGKV2
A,Cross-references: GDB:136265
A,Map position: 2p12-2p12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RTFGGGTKLEIK 132
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121 WTFGQGTKVEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :82-113/Region: framework 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 17/1
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             61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 MRLPAQLLGLLMLWVPGSSGDVVWTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Accession: 540324
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 2348-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Feference number: S40312; MUID:94080891; PMID:8258341
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-133 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 PAQFLFLLVLWIRETNGYVWTQTPLTLSVTIGOPASISCKSSQSLLDSDGKTYLNWLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 74.1%; Score 513; DB 2; Length 142; Best Local Similarity 74.0%; Pred. No. 2.7e-37; Matches 97; Conservative 16; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-142 < CHA>
A; Residues: 1-142 < CHA>
A; Cross references: EMBL:X56510
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 47-126/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;33-112/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: UNIPROT: Q8TCD0; EMBL: X72434
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132 FTFGOGTRLEI 142
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121 GQGTKVEIK 129
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S40324
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C'Species: Homo sapiens (man)
C'Daces: 29-401-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C'Daces: 22-401-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C'Accession: S22658
R'Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.
Nucleic Acids Res. 20, 261, 1992
A'Fitle: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-as A; Reference number: S22657; MUID:92285150; PMID:1598223
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWS 120
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                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                      Length 133;
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A;Rolecule type: mRNA
A;Residues: 1-140 AHTR>
A;Cross-references: UNIPROT:QBTCDD; EMBL:X59135
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heteroctetxamer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <816>
F:20-140/Product: 1g kappa chain (fragment) #status predicted <8
F:36-115/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                           19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain precursor V region (0-81VL) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.6%; Score 502.5; DB 2;
                                                                                                                                                                                                      Query Match 73.4%; Score 508; DB 1; Best Local Similarity 73.5%; Pred. No. 6.9e-37; Matches 97; Conservative 16; Mismatches 19
                                                             F;114-122/Region: complementarity-determining 3 F;123-133/Region: framework 4 F;43-113/Disulfide bonds: #status predicted
75-81/Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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RESULT 13

us-10-010-942b-2.rpr

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9
                                                1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
Best Local Similarity 73.7%; Pred. No. 2.2e-36;
Matches 98; Conservative 15; Mismatches 19; Indels
                                                                                                                          120 PRIFGGGTKLEIK 132
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121 PITFGQGTRLEIK 133
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A2452
19 kapa chain precursor V-II region (RPMI 6410) - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Date: 24-Jan-1988 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999
C;Accession: A24452
Nucleic Acids Res. 14, 3957-3970, 1986
A;Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.
A;Reference number: A24452; MUID:86232631; PMID:3086847

A;Molecule type: DNA X;Residues: 1-133 <WBI.> A;Cross-references: GB:M36859; NID:g185932; PIDN:AAA58920.1; PID:g185933 A;Note: this sequence was determined from the differentiated gene

A;Gene: GDB.1GKV2
A;Cross-references: GDB.136265
A;Cross-references: GDB.136265
A;Cross-references: GDB.136265
A;Cross-references: GDB.136265
A;Cross-references: GDB.136265
A;Cross-references: GDB.136265
A;Cross-reference: To a come cases, such as IgA and IgM, the subunits associate into la C;Complex: An immunoglobulin v region; immunoglobulin homology
C;Superfamily: immunoglobulin wrogloon; immunoglobulin homology
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-20/Domain: immunoglobulin v-II region (RPMI 6410) #status predicted <MAT>
F;36-115/Domain: immunoglobulin homology <IMM>
F;43-113/Disulfide bonds: #status predicted

Gaps ö, Query Match 71.7%; Score 496; DB 1; Length 133; Best Local Similarity 72.7%; Pred. No. 7.4e-36; Matches 96; Conservative 15; Mismatches 21; Indels 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW 60

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Search completed: September 26, 2005, 07:18:27 Job time : 26 secs

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; Sequence 164, Application US/09647468
; Patent No. 6677436
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121 TFGGGTKLEIK 131
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TYPE: PRT
ORGANISM: Mus sp.
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US-09-647-468-164
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  Query Match
Best Local 8
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Sequence 104, App
Sequence 102, App
Sequence 17, Appli
Sequence 12, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 119, Appli
Sequence 149, Appli
Sequence 54, Appli
Sequence 54, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 16, Appli
Sequence 11, Appli
                                                                                                                                               8 ; Search time 28 Seconds (without alignments) 351.917 Million cell updates/sec
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1 MMSPAQFLFLLVLWIRETNG......CWQGTHFPRTFGGGTKLEIK 132
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-647-68-164

US-09-497-625A-102

US-09-698-705-7

US-09-698-705-7

US-09-698-705-12

US-09-809-739-11

US-09-809-739-11

US-09-809-739-11

US-09-809-739-11

US-09-809-739-11

US-09-809-739-11

US-09-809-739-16

US-09-840-459-14

US-08-809-739-16

US-08-809-739-17
                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                  September 26, 2005, 06:29:58
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Maximum DB E
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No.
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Sequence 163, Application US/09647468

Sequence 163, Application US/09647468

Patent No. 6677436

GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
SOFTWARE FILING DATE: 1998-04-03
SOFTWARE PRESENCE: PROSE THAT SETON NUMBER: UP 10-91850
PRIOR FILING DATE: 1998-04-03
SOFTWARE PATON NUMBER: DELEGATION NUMBER: UP 10-91850
PRIOR FILING DATE: PATON NUMBER: UP 10-91850
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                                                   sequence
seq
sequence
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US-09-497-625A-15
US-09-809-739-15
US-09-840-625A-13
US-09-840-625A-13
US-09-840-625A-13
US-09-840-625A-106
US-09-809-739-18
US-09-809-739-18
US-09-840-459-107
US-09-840-459-107
US-09-497-655A-12
US-08-477-281A-84
US-08-477-2998-84
US-08-477-2998-84
US-09-940-625A-22
US-09-940-625A-22
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US-08-68-671-12
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Query Match
Best Local Similarity 93.5
Matches 115; Conservative
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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US-09-497-625A-102
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              APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDERI
APPLICANT: YABOCH, HOLBERI
APPLICANT: YABOCH, MACHINO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMANIZED ANTIBODY
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REPERBENGE: 503466/0289
CURRENT FILING DATE: 2000-09-29
PRIOR PELICATION NUMBER: DCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PARENTIN VET. 2.1
SEQ ID NO 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120
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COTHER INFORMATION: Description of Artificial Sequence: Amoino acid
COTHER INFORMATION: sequence coding for L chain V region of ant-TF
COTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-164
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APPLICANT: LAGORA, Gregory J.
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Reie, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ENGLOSE
TITLE OF INVENTION: METHODS OF USE THEREFOR
TITLE OF INVENTION: WHERE: US/09/840,459
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: US/09/97,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
NUMBER FO SEQ ID NOS: 107
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Patent No. 6696550
GENERAL INFORMATION:
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; ORGANISM: Mus musculus
US-09-840-459-102
GENERAL INFORMATION:
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ORGANISM: Mus sp.
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Patent No. 6824780
GENERAL INFORMATION:
APPLICANT: Devaux, B.
APPLICANT: Keller, G.
APPLICANT: Keller, G.
APPLICANT: APPLICANT: And Methods of Use
TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LLVLWIRETIGDVVMTQTPLTLSVTVGHPASISCKSSQSLLDSDGKTFLNWLLQRPGQSP
                                                                                                                                                                                                           70 KRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKL
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                                                                                                      10 LLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSP
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  Length 142;
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                                                    4; Indels
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APPLICANT: Largea, Gregory J.
APPLICANT: Largea, Gregory J.
APPLICANT: Newman, Walter
APPLICANT: Owner, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Reafe, Thereasa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REPERENCE: 1855.1052-004
FILE REPERENCE: 1855.1052-004
FURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/311,781
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR PILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SEQ ID NO 102
SEQ ID NO 102
87.6%; Score 606; DB 4;
93.5%; Pred. No. 8.4e-51;
iive 4; Mismatches 4;
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93.5%; Pred. No. 8.4e-51;
cive 4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 102, Application US/09497625A
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Matches 115; Conservative
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Sequence 11, Application US/09809739 Patent No. 6663863
                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.9%;
94.6%;
          GRAZIANO, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 105; Conservative
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OTHER INFORMATION: CDR3
OTHER INFORMATION: MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (55)...(61)
OTHER INFORMATION: CDR2
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSTLDS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Koeppen, H.
APPLICANT: Lasky, L.
TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use FILE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use FILE REPRENCE: P1777R1
CURRENT APPLICATION NUMBER: US/09/698,705
CURRENT APPLICATION NUMBER: US 60/162,558
PRIOR APPLICATION NUMBER: US 60/162,558
PRIOR PILING DATE: 1999-10-29
PRIOR PILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 25
SEQ ID NOS: 25
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                                                                                                                                                                                                                                                                                                    Length 113;
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                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-12
                                                                                                                                                                                                                                                                                             82.5%; Score 571; DB 4;
97.3%; Pred. No. 1.5e-47;
ative 2; Mismatches 1.
; FILE REFERENCE: P177R1; CURRENT APPLICATION NUMBER: US/09/698,705; CURRENT FILING DATE: 200-10-27; PRIOR APPLICATION NUMBER: US 60/162,558; PRIOR FILING DATE: 1999-10-29; PRIOR FILING DATE: 2000-02-16; NUMBER OF SEQ ID NOS: 25 SEQ ID NO 7.
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'Sequence 4' Application US/09203958A

'Patent No. 6682928

'GENERAL INFORMATION:
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Patent No. 6824780
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ORGANISM: Artificial sequence
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Best Local Similarity 97.34
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                       Best Local Similarity 97.3
Matches 108; Conservative
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APPLICANT: GOLDSTEIN, Joel
                                                                                                                                                                                                            TYPE: PRT ORGANISM: Mus musculus US-09-698-705-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Devaux, B.
Keller, G.
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                           LENGTH: 113
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OTHER INFORMATION: Murine mAb 1D9 light chain variable region NAME/KEY: STATE
LOCATION: (24)...(39)
OTHER INFORMATION: CDR1
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 81.2%; Score 562; DB 4; Length 353; Best Local Similarity 94.6%; Pred. No. 4e-46; Matches 105; Conservative 4; Mismatches 2; Indels
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APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia B.
TITLE OF INVENTION: Method of Inhibiting Stenosis and
TITLE OF INVENTION: Restenosis
TITLE OF INVENTION: Restenosis
TITLE REPERENCE: 1855.1069-003
CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT PILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR APPLICATION NUMBER: US 09/528,267
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASHSEQ for Windows Version 4.0
SEQ ID NO: 11
APPLICANT: DEC, Yashwant M.
TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
TITLE OF INVENTION: EXPRESSING ANTI-FC RECEPTOR
FILE REPERENCE: MAI-099CPA
CURRENT APPLICATION NUMBER: US/09/203,958A
CURRENT FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 60/067232
PRIOR APPLICATION NUMBER: 60/067232
PRIOR PILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 353
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Pred. No. 1.7e-46;
4; Mismatches 2
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GENERAL INFORMATION:
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US-09-647-468-149
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2 VVMTQTPLTISVTVGHPASISCKSSQSLLDSDGKTFLNWLLQRPGQSPKRLIYLVSKLDS 61
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| Sequence 9, Application US/09497625A
| Patent No. 6727349
| General INPORMATION:
| APPLICANT: LARVach, Christopher |
| APPLICANT: LARVach, Christopher |
| APPLICANT: Newman, Malter |
| APPLICANT: Ones, S. Tarran |
| APPLICANT: Ones, S. Tarran |
| APPLICANT: O'Reefe, Theresa |
| TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND |
| TITLE OF INVENTION: METHODS OF USE THEREFOR |
| TITLE OF INVENTION: METHODS OF USE THEREFOR |
| TITLE OF INVENTION: METHODS OF USE THEREFOR |
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| TITLE OF UNIVENTION: METHO
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APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1885.1022-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/197,625
PRIOR APPLICATION NUMBER: 09/197,625
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
NUMBER: O SEQ ID NOS: 107
PRIOR FILING DATE: 1999-07-23
NUMBER: PRESEC FOR WINGOWS VERSION 3.0
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Patent No. 6696550
GENERAL INFORMATION:
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US-09-840-459-9
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US-09-497-625A-9
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LENGTH: 112
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APPLICANT: SCHILLBERG, Stefan
APPLICANT: SCHILLBERG, Stefan
APPLICANT: SACK, Markus
APPLICANT: MONECKE, Michael
APPLICANT: MONECKE, Michael
APPLICANT: LIMAR SACK, Markus
APPLICANT: LIMAR SACK, Markus
APPLICANT: LIMAR SACK, Markus
APPLICANT: LIMAR SACK, Molecular Pathogenicide Mediated Plant Disease
TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
TITLE OF INVENTION: Resistance
TITLE OF INVENTION: Resistance
TITLE OF INVENTION: Resistance
TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
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TITLE OF INVENTION: Molecular Plant Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic,
; OTHER INFORMATION: natural origin
US-09-419-788-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPHTFGGGTKLEIK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQCTHFPYTFGGGTKLEIK 112
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                                                                                                                                                                                                                                                                                                                                                                                          Length 112;
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                                                                                                                                                                                                                                                                                                                                                                                80.9%; Score 560; DB 4; Length 11
94.6%; Pred. No. 1.7e-46;
ive 4; Mismatches 2; Indels
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-497-625A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 113, Application US/09419788 Patent No. 6825325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 149, Application US/09647468 Patent No. 6677436
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                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.6'
Matches 105; Conservative
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62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPDTFGGGTKLEIK 112
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; Sequence 54, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
                                                                                                                                                                                                         Sequence 54, Application US/09840459 Patent No. 6696550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 92.8
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-840-459-54
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APPLICANT: SATO, KOH

APPLICANT: ADACHI, HIDEKI

APPLICANT: ADACHI, HIDEKI

APPLICANT: ADACHI, HIDEKI

APPLICANT: ADACHI, HIDEKI

TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY

FILE REFERENCE: 05346(0.289)

CURRENT APPLICATION NUMBER: US/09/647,468

CURRENT PILING DATE: 1999-04-02

PRIOR FILING DATE: 1999-04-02

PRIOR PLING DATE: 1999-04-03

NUMBER OF SEQ ID NOS: 183

SOFTWARE: PALCHIN VOL. 2.1

SEQ ID NOS: 183
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: ADACHI, HIDEKI
APPLICANT: ADACHI, HORNIE
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMANIZED ANTIBODY
TITLE OP INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REPERBENGE: 633466/0289
CURRENT FILING DATE: 2000-09-29
PRIOR PELICATION NUMBER: DCT/JP99/01768
PRIOR PELICATION NUMBER: PCT/JP99/01768
PRIOR PELICATION NUMBER: DT 10-91850
PRIOR PELICATION NUMBER: JP 10-91850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mus sp.
PEATURE:
OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
US-09-647-468-149
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US-09-647-468-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 VVLTQTPLTLSVTIGQPASVSCKSSQSLLDSDGKTYLLNWLLQRPGQSPKRLIYLVSKLDS 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 150, Application US/09647468
Patent No. 6677436
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Matches 105; Conservative
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US-09-647-468-150
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GENERAL NO. 0895301
GENERAL NO. 0895301
GENERAL NO. 0895301
APPLICANT: LAROSA, Gregory J.
APPLICANT: HORVARITON:
APPLICANT: HOWANAI, Christopher
APPLICANT: O'Reien, Siobhan H.
APPLICANT: O'Reien, Siobhan H.
APPLICANT: O'Reien, Siobhan H.
APPLICANT: O'Reien, BUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
NUMBER: OF SEQ ID NOS: 107
SOFTWARE: PRECED NOS: 107
SOFTWARE: PRECED NOS: 107
SOFTWARE: PRECED NOS: 107
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APPLICANT: LARGEA, Christopher
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Owner, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Refe, Thereas
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
TITLE OF INVENTION WHERE: 09/497,625A
CURRENT FILING DATE: 2000-02-03
PRIOR PRILICATION NUMBER: 09/121,781
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR APPLICATION NUMBER: 09/121,781
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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92.8%; Pred. No. 4e-46;
tive 7; Mismatches
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Query Match

80.3%; Score 556; DB 4; Length 112;
Best Local Similarity 92.8%; Pred. No. 4e-46;
Matches 103; Conservative 7; Mismatches 1; Indels
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-497-625A-54
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Gaps

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Search completed: September 26, 2005, 07:19:02 Job time: 29 secs

sequence 5, Appli sequence 11, Appl sequence 11, Appl sequence 11, Appl sequence 11, Appl sequence 52, Appl sequence 52, Appl sequence 61, Appl sequence 61, Appl sequence 102, Appl sequence 11, Appli sequence 11, Appli sequence 1, Appli

Sequence:

Run on:

Searched:

Database

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MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
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; Sequence 2, Application No. US20030165496A1
; GENERAL INFORMATION:
    APPLICANT: Basi, Guriq
; APPLICANT: Basi, Guriq
; APPLICANT: Sedach, Jose
; TITLE OF INVENTION: BETA ANYLOID PEPTIDE
; TITLE OF INVENTION: BETA ANYLOID PEPTIDE
; TITLE OF INVENTION: BETA ANYLOID PEPTIDE
; CURRENT FILING DATE: 2002-12-06
; PRIOR FILING DATE: 2002-12-06
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO
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100.0%; Pred. No. 6.4e-57;
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US-10-704-705-5
US-10-232-030-5
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US-10-388-389-11
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US-10-704-773-11
US-10-232-030-11
US-10-899-58
US-10-830-899-58
US-10-830-899-58
US-10-861-662-58
                                                                                                                                                                                                                                     US-09-840-459-102

US-10-766-773-102

US-10-76-610-102

US-10-733-563-102

US-10-937-046-7

US-10-937-046-12

US-10-937-046-12

US-09-203-958A-4

US-09-840-459-9
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US-10-766-610-9
US-10-733-563-9
US-10-855-013-12
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)...(20) US-10-010-942B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 132; Conserv
   NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-010-942B-2
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Sequence 164, App
Sequence 19, Appl
Sequence 49, Appl
Sequence 5, Appli
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(without alignments)
103.124 Million cell updates/sec
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Sequence 2, A
Sequence 2, A
Sequence 2, A
Sequence 2, A
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 US-10-38B-2

1 US-10-703-713-2

1 US-10-704-070-2

1 US-09-881-823-10

1 US-09-881-823-10

1 US-10-462-062-164

2 US-10-462-062-164

3 US-10-942B-5

1 US-10-942B-5
                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                     1826554 segs, 407025358 residues
                                                                                                       September 26, 2005, 07:14:55
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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Sequence 86, App. Sequence 88, App.

Sequence 12, Sequence 9, Sequence 9,

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Result Š 9

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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 132
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Best Local Similarity 100.0
Matches 132; Conservative
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                                                                                                                                                                  TYPE: PRT
ORGANISM: Mus musculus
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; LOCATION: (1) ... (20)
US-10-704-070-2
                                                                                                                                                                                                                                      ; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-703-713-2
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                                LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                        61 LLQRPGOSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIRAEDLGLYYCWGGTHFP 120
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Sequence 2, Application US/10703713

Publication No. US20040171815A1

GENERAL INFORMATION:

APPLICANT: Baldanha, Jose

APPLICANT: Saldanha, Jose

APPLICANT: Yednock, Ted

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

CURRENT APPLICATION NUMBER: US/10/33,713

CURRENT FILING DATE: 2003-11-07

PRIOR FILING DATE: 2003-03-12

PRIOR PELICATION NUMBER: US/10/388,389

PRIOR FILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US 60/251,892

PRIOR FILING DATE: 2000-12-06
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                                                                                                                                                                                                             121 KTFGGGTKLEIK 132
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ORGANISM: Mus musculus
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; LOCATION: (1)...(20)
US-10-388-389-2
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100.0%; Score 692; DB 16; Length 132; 100.0%; Pred. No. 6.4e-57; tive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10704070
; Sequence 2, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704
; CURRENT FILING DATE: 2003-11-07
; PRIOR FILING DATE: 2003-11-07
; PRIOR FILING DATE: 2003-12-06
; PRIOR FILING DATE: 2001-12-06
; PRIOR FILING DATE: 2001-12-06
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ. ID NOS: 63
; SOFTWARE: FRAESEQ for Windows Version 4.0
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Query Match 93.9%;
Best Local Similarity 93.2%;
Matches 123; Conservative
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; ORGANISM: Murine US-09-881-823-10
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US-10-462-062-164
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APPLICANT: CHEN, LI
TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
TITLE OF INVENTION: WHERE: US/09/881,823
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR APPLICATION NOS: 32
SOFTWARE: PATENT HOS: 32
SOFTWARE: PATENT NESTED NOS: 32
SOFTWARE: PATENT NESTED NOS: 32
LENGTH: 135
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                                                                                                       Sequence 2, Application US/10232030
Publication No. US20050009150A1
GENERAL INPORMATION:
APPLICANT: Dale Schenk
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
FILE REFERENCE: ELM-002CM
CURRENT FILING DATE: 1002-08-30
CURRENT FILING DATE: 2002-08-30
PRIOR FILING DATE: 1998-11-30
PRIOR PRIOR TILING DATE: 1998-11-30
PRIOR PLILING DATE: 1999-05-28
PRIOR FILING DATE: 1999-05-28
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-2-06
PRIOR PLICATION NUMBER: US 10/010,942
PRIOR FILING DATE: 2001-12-06
PRIOR PLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2001-12-06
PRIOR FILING DATE: 2001-13-06
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100.0%; Pred. No. 6.4e-57;
tive 0; Mismatches 0;
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Patent No. US20020068066A1
GENERAL INFORMATION:
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APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
APPLICANT: WIMS, LETITIA
APPLICANT: CHEN, LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 132; Conservative
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; LOCATION: (1)...(20)
US-10-232-030-2
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US-09-881-823-10
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APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: ADACHI, HIDEKI
APPLICANT: ADACHI, HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: 92704-02
PRIOR APPLICATION NUMBER: 92704-02
PRIOR APPLICATION NUMBER: J999-04-02
PRIOR PLING DATE: 1999-04-03
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
SOFTWARE OF SEQ ID NOS: 183
SOFTWARE PALENTING DATE: 2.1
SEQ ID NO 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
OTHER INFORMATION: antibody ATR-7
US-10-462-062-163
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                                                                                                                                                                                                                                                       61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYXCWQGTHFP 120
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; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
                                                                                                                                                61 LLORPGOSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP
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                                                                                                               1 MMSPAQPLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
                                                          0; Gaps
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Score 650; DB 9; Length 135;
Pred. No. 5.6e-53;
5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 163, Application US/10462062
Publication No. US20040044187A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                             121 RTFGGGTKLEIK 132
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121 LTFGAGTKLELK 132
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Subjection US/10810881A

Subjection No. US20050128695A1

Fublication No. US20050128695A1

GENERAL INFORMATION:

APPLICANT: Mercken, Marc; Benson, Jacqueline M.

TITLE OF INVENTION: ANTI-AMYLOID ANTIBODIES, COMPOSITIONS, METHODS AND USES

FILE REFRENCE: CENSO21 NP

CURRENT APPLICATION NUMBER: US/10/810,881A

CURRENT FILING DATE: 2004-03-26

PRIOR APPLICATION NUMBER: US 60/458,469

PRIOR PILING DATE: 2003-03-28

PRIOR PILING DATE: 2003-03-28

PRIOR PILING DATE: 2003-03-28

PRIOR FILING DATE: 2003-03-38

PRIOR FILING DATE: 2003-03-38

PRIOR PLICATION NUMBER: US 60/458,510

PRIOR PLICATION NUMBER: US 40/458,510

PRIOR 49
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Best Local Similarity 91.7%; Pred. No. 3.8e-52;
Matches 121; Conservative 6; Mismatches 5;
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OTHER INFORMATION: Signal Peptide
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NAME/KRY: MISC FEATURE
COCATION: (123)...(133)
US-10-810-881A-49
  121 RTFGGGTKVEIK 132
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LOCATION: (75)...(81)
OTHER INFORMATION: CDR2
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OTHER INFORMATION: CDR3
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OTHER INFORMATION: CDR1
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NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: FR2
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OTHER INFORMATION: FR3
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OTHER INFORMATION: FR1
FEATURE:
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NAME/KEY: MISC_FEATURE
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NAME/KEY: SIGNAL
                                                                                                    US-10-810-881A-49
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NAME/KEY: 1
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                                                                                                                                                                                                                                                                                                                                                               FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
CTHER INFORMATION: Sequence for L chain V region of anti-TF mouse monoclonal
CTHER INFORMATION: antibody ATR-8
US-10-462-062-164
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AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
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93.4%; Score 646; DB 15;
Best Local Similarity 93.1%; Pred. No. 1.3e-52;
Matches 122; Conservative 5; Mismatches 4;
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Pred. No. 3.9e-52;
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                     FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
FRIOR APPLICATION NUMBER: PCT/JP99/01768
FRIOR FILING DATE: 1999-04-02
FRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 164
LENGTH: 131
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Publication No. US20050090648A1
GENERAL INFORMATION:
APPLICANT: E1 Lilly and Company
TITLE OF INVENTION: Humanized Antibodies
FILE REFERENCE: X14958
CURRENT APPLICATION NUMBER: US/10/476,265
CURRENT FILING DATE: 2003-10-22
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 239
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; OTHER INFORMATION: humanized antibody
US-10-476-265-19
                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 90.9%;
Matches 120; Conservative
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  TITLE OF INVENTION:
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US-10-476-265-19
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; Sequence 5, Application US/10704070
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NAME/KEY: SIGNAL
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US-10-704-070-5
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US-10-703-713-5
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CTHER INFORMATION: humanized 3D6 light chain variable region US-10-010-942B-5
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Sequence 5, Application US/10388389
Publication No. US20040087777A1
GENERAL INFORMATION:
APPLICANT: Basi, Gurid
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
FILE REFERENCE: ELN-002CP
CURRENT PRILICATION NUMBER: US/10/388,389
CURRENT PILING DATE: 2003-03-12
PRIOR PILING DATE: 2001-12-06
PRIOR PILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 132
                                                                                                                                                                                                                     APPLICANT: Basi, Guriq
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: HUMANIZED ANTIOLD PEPTIDE
FILE REFERENCE: ELN-002
CURRENT APPLICATION NUMBER: US/10/010,942B
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR PILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FRESEQ FOR Windows Version 4.0
                                                                                                                                                          Sequence 5, Application US/10010942B Publication No. US20030165496A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
PEATURE:
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                                 121 RTFGGGTNLEIK 132
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|21 RTFGOGTKVEIK 132
121 RTFGGGTKLEIK 132
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                                                                                                                                    US-10-010-942B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5
LENGTH: 132
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                                                                                                                                                                                                                                                                      1 MMSPAQFLFLLVLWIRETNGYVVMTQSPLSLPVTPGEPASISCKSSQSLLDSDGKTYLNW
                                                                                                                                                                                                                                    1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
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                                                                                                                   Length 132;
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region US-10-388-389-5
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; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-703-713-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/10703713
; Sequence 5, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
    APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AWTLOID PEPTIDE
; TITLE OF INVENTION: BETA-AWTLOID PEPTIDE
; TILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT PLIING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 10/10,942
; PRIOR PLIING DATE: 2000-12-06
; RUMBER OF SEQ ID NOS: 63
; SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                             Query Match 92.5%; Score 640; DB 15; Length 1 Best Local Similarity 90.2%; Pred. No. 4.7e-52; Matches 119; Conservative 10; Mismatches 3; Indels
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ORGANISM: Artificial Sequence
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LOCATION: (1)...(20)
OTHER INFORMATION: humanized 3D6 light chain variable region
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publication No. US2005009150A1

GENERAL INFORMATION:
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: HETA-AMYLOID PEPTIDE
FILE REFERENCE: ELN-002CN
CURRENT APPLICATION NUMBER: US/10/232,030
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 09/201,430
PRIOR APPLICATION NUMBER: US 09/201,430
PRIOR APPLICATION NUMBER: US 09/201,430
PRIOR APPLICATION NUMBER: US 09/22,289
PRIOR FILING DATE: 1999-01-27
PRIOR FILING DATE: 1999-05-28
PRIOR PLING DATE: 1999-05-28
PRIOR PLING DATE: 1999-05-28
PRIOR PLING DATE: 2000-11-06
PRIOR FILING DATE: 2000-12-06
PRIOR FILING DATE: 2000-12-06
PRIOR FILING DATE: 2000-12-06
PRIOR FILING DATE: 2000-12-06
PRIOR PLING DATE: 2000-12-06
PRIOR PLING DATE: 2000-12-06
PRIOR FILING DATE: 2000-12-06
                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
Publication No. US20040171816A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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US-10-232-030-5
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AGENCOURT
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BF301241
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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BF105366
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CO565696
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BM758592
BU930837
BU759427
AW405187
CD699289
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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396
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Perfect score:
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CD695306 EST11829 CD702671 EST19196 CB99522 AGENCOURT CD699812 EST16336 CD690641 EST71634 h CD700169 EST16693 CB985900 AGENCOURT CD707996 EST2520 h CD69298 EST2520 h BG547597 602575437 CB9877308 AGENCOURT CB987308 AGENCOURT CB987308 AGENCOURT CB987794 EST3820 h CB987794 CBCCOURT CB987645 AGENCOURT CB987645 AGENCOURT CB987645 AGENCOURT CB987641 AGENCOURT CB987641 AGENCOURT CB987641 AGENCOURT CB987641 AGENCOURT CB987641 AGENCOURT	ENTS	BG954451 M 602812101F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4986529 5', mRNA sequence. B0594451. G1:14352088 BNA musculus (house mouse) Mus musculus (house noin in i	368.8; DB 4; Length 773; No. 1.9e-105; smatches 17; Indels 0; Gaps 0;
CD695306 CD702671 CD8985229 CD6906812 CD6906812 CD700169 CD70010906 CD70010906 CD70010906 CD8982398 CD689298 CD689298 CG6987595 CD6987595	ALIGNMENTS	TIFI NCI_CGAP_CO24 Mus muss Juence. L.1 GI:14352088 unlus (house mouse) unlus (house mouse) a; Metazoa; Chordata; Crara a; Eutheria; Rodentia; Scita a; Lo 773) http://mgc.nci.nih.gov/. Institutes of Health, Man http://mgc.nci.nih.gov/. Institutes of Health, Man and (1999) Robert Strausberg, Ph.D. Gagabs.r@mail.nih.gov Procurement: Jeffrey E. Gre Ebrary Preparation: Life I.M puencing by: Incyte Genomic puencing by: Incyte Genomic puencing by: Incyte Genomic listribution: MGC clone dis brough the I.M.A.G.E. Conse inage.llnl.gov Location/Qualifiers 1. 773 / organism="Mus musculus" / mol.type="musNa" / strain="FVB/N" / db.xref="taxon:10090" / clone lib="NCI CGAP_CO22 / clone lib="NCI CGAP_CD22 / clone lib="NCI CGAP_CO22	Score Pred. 0, Mi
^		CGAP. 143520 100 113; F. 1733 101 100 113; F. 1733 101 100 113; F. 1733 102 103; F. 173 103 103; F. 173 104 105; F. 173 105 105; F. 17	93.1%; 95.7%; ive
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Gaps .. 120

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/db xref="taxon:10090"
/db xref="taxon:10090"
/clone="INAGE:4164906"
/lab_host="DH10B (TI phage-resistant)"
/clone lib="NCI GAP_SG2"
/note="Organ: salivary gland; Vector: pGNV-SPORT6; Site 1:
Not!; Site_2: Sali, Cloned unidirectionally. Primer: Olīgo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF301241 10V-2000 02029676F1 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4164906 5',
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                                                                                                  7 Argarcagreccagreccagrecrerrecracecrerecarreaaaaccaacgr
                                                                                                                                      61 TATGTTGTGATGACCCAGACTCCACTCTTGTCGGTTACCATTGGACAACCAGCCTCC
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                      Indels
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Pred. No. 7.2e-102;
0; Mismatches 24;
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/mol_type="mRNA"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence. BF301241
BF301241 GI:11247764
  93.98;
                      372; Conservative
    Best Local Similarity
                                                                                                                                                                                                                                                                                                181
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602893669F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5038576 5',
                                                                                                                                        180
                                                             120
                                                                                                  73 GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 132
                                                                                                                                                             133 ATCTCTTGCAAGTCCAGGGCCTCTTAGCTGGTGATGGAAACACATTTTTGAATTGG 192
                                                                                                                                                                                                                    181 TIGITACAGAGGCCAGGCCAGICTCCAAAGCGCCTAAICTAICTGGIGICTAAACTGGAC 240
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                                                                                                                                                                                                                                                                                                                        253 TCTGGAGTCCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTTCACACTGAAAATC 312
                                                                                                                                                                                                                                                                                                                                                                             301 AGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT 360
                                                                                                                                                                                                                                                                                                                                                                                                      313 AGCAGAGTTGAGGCTGAGGATCTGGGAGTTTATTGCTGGCAAGGTACACATTTTCCT 372
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 919)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: egapbe-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: MGC Clone Gistribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAMI1106 row: j column: 17
High quality sequence stop: 834.
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/tissue type="spontaneous tumor, metastatic to mammary.
/tissue type="spontaneous tumor, metastatic to mammary.
/tissue type="spontaneous tumor, metastatic to mammary."
/lab host="norign"
/clone lib="NCI CGAP Lu29"
/note="forgan: lung; Vector: pCMV-SPORT6; Site 1: SalI;
/site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                      72
121 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.3%; Score 357.6; DB 4; Length 909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 CGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 CAAACGITCGGIGGAGGCACCAAGCIGGAAAICAAA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
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Email: cgapbs-remail.nih.gov
Tissue Procurement: John C. Marshall, M.D., Ph.D
Tissue Procurement: John C. Marshall, M.D., Ph.D
CDNA Library Preparation: CLOWIECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3149 row: n column: 08
High quality sequence stops: 568.
Location/Qualifiers
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AGENCOURT 11790259 NICHD Rr Bit1 Rattus norvegicus cDNA clone
IMAGES6890409 5', mRNA sequence.
                                                                                                                                                                                                                                                        160 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAAT--G 217
                                                                                                                                                                                                                                                                                                            181 TIGITACAGAGGCCAGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGAC 240
                                                                                                    61 TATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 120
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
                                                                              1 ATGATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_hogt="DH10B"
/clone_lib="NICHD_Rr_Pit1"
/note="Vector: pDNR-LIB; Site_1: Sfi1; Site_2: Sfi1;
                                            Gaps
                                        7;
      Length
                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GGACGTTCGGTGGAGCACCAAGCTGGAAATCAAA 431
    DB 2;
    Score 312.4; DB 2
Pred. No. 1.6e-87;
0; Mismatches 6
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/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
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/tissue_type="Pitutary"
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CB316492.1 GI:28840727
Query Match
Best Local Similarity 96.7%;
Matches 383; Conservative
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CB316492
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Musucities and Caralata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 407)

Si Acazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaqi, K., Tomaru, Y., Hanegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Corbani, L. B., Cousins, S., Dalla, B., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazer, K. S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gariboldi, M., Gassi, C., Godzik, A., Gough, J., Grimmond, S., Kanasi, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numack, K., Okido, T., Pavan, W. J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGCGCAATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.23 kb (range 0.5-4.0 kb). 15/15 colonies contained inserte by PCK. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 TTATTACAGAGTCCTGGCAGGTCTCCGAAGCGCCTAATCTATCAGGTGTCTAATCTGGGC
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                                                                                                                                                                                                                                                                                                                                                             Score 311.2; DB 6
Pred. No. 3.6e-87;
0; Mismatches 53
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Mus musculus
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Best Local Similarity 86.6%;
Matches 343; Conservative
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BY344116 BIKEN full-length enriched, whole joints Mus musculus CDNA clone L730002K22 5', mRNA sequence.
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                                                              ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGG 180
                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                  241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC
                                                                                                                                                                                                                                                                                                                                       301 AGCAGAATAGAGGCTGAGGATTTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT
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Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walla, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yana, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Xonno, H., Nakamura, M., Arakawa, T., Fukawa, T., Konno, H., Nakamura, M., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Saski, M., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-reseases.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramateu,M. and
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Computational Analysis of Full-Length Mouse cDNAs Compared with
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Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1677-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 34 multicapillary sequencer. Genome Res.
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                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/clone_lib="RIKEN full-length enriched, activated spleen"
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/mol_type="mRNA"
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/clone="F830301N12"
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           Email: genome-reseggec.riken.jp, URL:http://genome.gec.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., imctani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Nakai,K., Watahiki,A., Muramateu,M. and
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Normalization and subtraction of cap-trapper-selected cDNAs to
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
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Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences
Research Center 'Al. Pleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari,Greece | whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCT 150
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urther details.
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/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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/organism="Mus musculus"
/mol_type="mRNA"
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AZ938720 618 bp DNA linear GSS 26-APR-2001 2M0197H20F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

AZ938720 LOCUS DEFINITION

RESULT 7

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAQ-2 (gil #1732114 [gb] API-29072.1); a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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/clone llb="Mouse 10kb plasmid UUGCZM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C578L/67 (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 618)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Rallan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="UUGC2M0197H20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
                                                           Mus musculus (house mouse)
Mus musculus
AZ938720.1 GI:13798758
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Plate: 0197 row: H o
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Unpublished (2000)
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Fax: 801 585 7177
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301 AGCAGAATAGAGGCTGAGGATTTGGG
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/strain="NOD"
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Best Local Similarity 95.1%;
Matches 310; Conservative 0
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Colosaci, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido; I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, A.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, A.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Mogami, A.,

Butalov, S., Balsel, K., Blake, J.A., Bradt, D., Bult, C.,

Garibold, M., Gissi, C., Godaik, A., Gough, J., Grimmond, S.,

Gariboldi, M., Gissi, C., Godaik, A., Gough, J., Grimmond, S.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B. D., Konagaya, A.,

Kurochkin, I.V. Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Munata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,

Ravasi, T., Reed, J.C., Reed, D.J., Renachandran, S.,

Ravasi, T., Red, J.C., Reed, D.J., Setou, M., Shimada, K.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Tarkenaka, Y., Taylor, M.S., Teasdale, R.D., Tonita, M.,

Verardo, R., Wagner, L., Wanbaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yana, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Banney, E. and Hayashizaki, Y.

Rogers, J., Band, S., Hara, A., Hashizume, W., Imotainal annotation

of 60,770 full-length consa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY216837 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830047E03 5', mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
                                                                                                                                                                                            342
                                                                                   282
                                                                                                                                                                                                                     Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
                                                                                                                                     408 CTGGTGTCTAAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACA
                                                                                                                                                                                            GATTTTACACTGAAAATCAGCAGAATAGAGGCTGAGGATTTGGGAACTTTATTATTGCTGG
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                   343 CAAGGTACACATTTTCCTCGGAC 365
                                                                                                                                                                                                                                                                                                                                                     528 CAAGGTACACATTTTCCTCACAC 550
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BY216837
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Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computation Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mam. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraties for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust/Mac Centre for Molecular Mechanisms in Disease Wellcome Trust/Mac Centre for Molecular Mechanisms in Disease Wellcome Please visit our web site (http://genome.gsc.riken.go.jp) for Loarion/Onalifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF134462
601784859F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4012790 5',
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/tissue type="activated spleen"
/clone lib="RIKEN full-length enriched, activated spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TATGTTGTGATGACCCAGACTCCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 ATGATGAGTCCTGCCCAGTTCCTGTTTCTGCTAGTGCTCTCGATTCAGGAAACCAACGGT
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                                                                Is numerated to 883)

In the McC http://mc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://mage.lln.gov

Plate: LLAM9254 row: e column: 15

High quality sequence stop: 708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /notes=Torgan: ling; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: Sal1; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 GATG-TGTGATGACTCAGACCCCACTCAC-TTGTCGGTTACCA-TGGACAACCAGCCTCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ATCTCTT-GCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 CTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAAT 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 ATCTCTTGGCAAGTCAAGTCAGAGCCTCTTACATAGTAATGGAAAGACATATTTGAA-TG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 Griatiacadadeceadeceadrereceaadereceaarerateraterateraaacrega 254
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                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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Matches 374; Conservative
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BY216432 BIXEN full-length enriched, activated spleen Mus musculus CDNA clone F830044L02 5', mRNA sequence.

LOCUS

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Mus Muscalus Butheria; Rodentia; Sciurognath; Muridae; Mutinae; Muscalus Butheria; Rodentia; Sciurognath; Muridae; Mutinae; Muscalus I (bases I to 346)

1 (bases I to 346)

2 (bases I, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kayazaka, T., Tomaru, Y., Hasegawa, Y., Mogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Riyosawa, H., Baldarelli, R., Hill, D.P., Bult, C., Corbani, L.B., Cousine, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Farzer, K.S., Gaasterland, T., Chothia, C., Corbani, L.B., Frazer, K.S., Gaasterland, T., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanaj, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Multais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Kamachandran, S., Ravasi, T., Raed, J.C., Reed, J.G., Reed, J.G., Ramachandran, S., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Schneider, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Watlana, R., Zake, Mar, A., Carninci, P., Hayateu, N., Sato, K., Sato, K., Kawai, J., Alzawa, K., Shinayawa, R., Yasunishi, A., Sathi, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Sathi, K., Sasaki, D., Sato, Shibata, K., Shinayawa, R., Yasunishi, A., Sathi, K., Sasaki, D., Sato, K., Shinayasi, A., Sasaki, A., S
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
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Mus musculus (house mouse)
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/db_xref="taxon:10090"
/clone="F830044102"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 GATGTTGTGATGACTCAGACCCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271 TCTGGAGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATC 330
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                             for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp)
further details.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                              73.3%; Score 290.4; DB 5; Length 346; 94.9%; Pred. No. 1.1e-80; ive 0; Mismatches 16; Indels 0
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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Broyelopedia Project of Genome Exploration Research Group in Riken
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Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wining, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yang, L., Yang, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakaume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Myazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, B. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Best Local Similarity 94.9%; Pred. No. 1.1e-80;
Matches 300; Conservative 0; Mismatches 16
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Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Shibata, K., Shibata, K., Shibata, K., Shiri, Y., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

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RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (10), 1617-1630 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Computer-based methods for the mouse Full-length cDNA encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Trust/MRC building Addenbrokes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for farther for the full of the professing to the state of the content o
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216
Email: genome-res@gec.riken.jp, URL:http://genome.gec.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                        271 TCTGGAGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATC 330
                                                                                                                                                                                                                        TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
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DEFINITION
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BY217354
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KEYWORDS
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BY215445
BY215445 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830037C03 5', mRNA sequence.
BY215445.1 GI:26396173
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                                                                                                                                                                                                                                                                                                                                                                   61 TATGTTGTGATGACCCAGACTCCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 120
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/tissue_type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"
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                                                                                                                  72.8%; Score 288.2; DB 5; Length 355; 92.9%; Pred. No. 5.8e-80; ive 0; Mismatches 23; Indels 0
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TITLE

COMMENT

ORGANISM

KEYWORDS

REFERENCE AUTHORS

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    .342
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="NOD"

                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY346516.1 GI:26576004
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Matches 295; Conservative
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further details
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BY346516
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                                            FEATURES
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S. Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Riyoawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Riyoawa, H., Balkel, Y., Hall, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batsel, K., W., Blake, J.A., Hill, D.P., Bult, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Glasi, C., Gorbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Gustincich, S., Hirokawa, N., Jackson, J.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzlerski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzlerski, R.M., King, B.L., Konagaya, A., Maltais, L., Marchionni, L., MoKenis, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petole, G.,
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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishli,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of captrapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKSI integrated sequence analysis (RIGA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RikEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Vokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
T-722 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
                                    Mus musculus (house mouse)
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MEDLINE PUBMED COMMENT

JOURNAL

TITLE

prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose

assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for

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BST.

Mus musculus (house mouse)

BUKaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

BUKaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus musculus

BUKaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus .

1 (bases 1 to 312)

8 (Aszaki, Y., Futuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Golobori, T., Baldarelli, K., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schhriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothaii, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Fazzer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Pevran, W.J., Pertea, G., Pesole, G., Petroveky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Relid, J., Ring, B.Z., Ringwald, M., Sahaeilin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Saltana, R., Takenaka, Y., Taylor, M.S., Teardale, R.D., Tomita, M., K., Verardo, R., Wange, Y., Wange, Y., Wang, Y., Wange, 
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151 Arcrictriccaaarcaagricagagcccrirracaragraarggaaagacararrigaarrig 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GITGITACAGAGGCCAGGCCAGICTCCAAAGCGCCTAAICTAICTGGTGICTAAACTGGA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 ATCTGGAGTCCCCTGACAGGTTCAGTGGATGATCAGGGACAGATTTCACACTGAAAT 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 CTCTGGAGTCCCTGACAGGTTCACTGGCAGTGGGATCAGGGACAGATTTTACACTGAAAAT 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                               DB 5; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                         Score 274.4; DB 5;
Pred. No. 1.4e-75;
0; Mismatches 16;
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/mol_type="mRNA"
/db xref="taxon:9606"
/clone="InAGE:6215018"
/lab host="DH10B (phage-resistant)"
/clone=lib="NHH MGC_113"
/clone=lib="NHH MGC_113"
/clone="Crgan: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: note="Organ: spleen; Vector: poTB7; Site 1: XhoI; Site 2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                       960 bp mRNA linear EST 16-JUL-2002
AGENCOURT 7975525 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215018
BQ711007
   151 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTATATAGTAATGGAAAAACCTATTTGAATTGG 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 960)

NIH-MGC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-ramail.nih.gov
Tissue Procurement: Dr. Mark Watson
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2181 row: e column: 03
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High quality sequence stop: 462.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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Best Local Similarity 79.0
Matches 313; Conservative
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-res@gc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozani,F., Imbial,Y., Ishii,Y., Itch,M., Kawai,J., Konno,H.,
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
connucleur-based methods for the mouse Eull-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Exploration Research Group in Riken
Division of Experimental Animal Research in Riken contributed to
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,I., Yang,I., Yana,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatteu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Alzawa,K., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Alzawa,K., Arakawa,T., Pukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,T., Miyazaki,A., Sasaki,K., Sasaki,D., Shibata,K., Shinaqawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,B.S., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60, 770 full-length cDNas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 GATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCT 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Pleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 ATGATGAGTCCTGACCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCAGGAAACCAACGGT
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further details.
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/db xref="taxon:10090"
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/clone_lib="RIKEN full-length enriched, whole joints"
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                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Db 183 TACCTGCAGACCAGCCTCCCACAGCTCCTGATCTATGCAGCTTC 242

Qy 241 TCTGCAGTCCCTGACAGCTTCATGCGCACACATTTACACTCAAAATC 300

243 TCTGCAGTCCCTGACAGCTTCACTGCGCAGCACACATTTTACACTCAAAATC 300

243 TCTGCAGTGCCAGATTAGGCAGCGGCTCAGGCACAGATTTCACACTCAAAATC 302

Qy 301 AGCAGAATAGAGGTTAGGACTTTATTATTGCTGGCAAGGTACATTTTCCT 360

Db 303 AGCCGGTGAGGCTGAGGATTTGGAGTTTATTATTGCTGCAAGGTACAATTTTCCT 362

Qy 361 CGCAGTTCGGTGAGGTTTGTGGAGTTTATTATTGCTGCAAGTATACAGTTTCCT 362

Qy 361 CGCAGTTCGGTGAGGTTGAGGTTGATACTGCATGCAAGTATACAGTTTCCT 362

Qy 361 CGCACTTCCGTGAGGCTCAAGCTGCAAAGTATACAGTTTCCT 362

Db 363 CTCATTTCGGCGAGGGACGAAGGTCAAA 398

Search completed: September 26, 2005, 06:27:24

Job time: 2364 8ecs
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Abs59426 Mouse 3D6
Adp45590 Mouse bin
Abn84610 Anti-Stre
Adm72032 Chimeric
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Adm72034 Chimeric
Aax58916 Plasmid p
Aad25665 Sequence
Acc84730 Mouse MAb
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Abz34634 Humanised
Aaz33016 Anti-tiss
Aaq12063 Sequence
Aaq12019 Sequence
Abx16570 Mouse DNA
Aaq5691 Sequence
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                 4390206 seqs, 2959870667 residues
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Maximum Match 100%
Listing first 45 summaries
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ADP45590
ABM9610
ADM72032
ABZ24632
ABZ24634
AAZ33016
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	O١	A77		Murine	Aav36236 DNA of Sc			Ads17377 Nucleotid	Aah21232 Murine de	Coding	Aag20307 B cell hy	Σ	Add05269 Female mo	Adm80360 Murine ho	Aat86234 Anti-huma	Aat86221 Human p53	Adi26468 Murine I4	7	Abk15814 DNA encod	Aaa62120 Mouse HBV	Aah77316 IgG Fab-B	Aat86646 Mus muscu	Aax58687 Monoclona	Aai70097 Type II c	
	ADE06759	AAV20601	AAF74891	AAD15262	AAV36236				AAH21232	-	AAQ20307	ACF79290	ADD05269	ADM80360	AAT86234	AAT86221	ADI26468	ADE13217	ABK15814	AAA62120	AAH77316	AAT86646	AAX58687	AAI70097	
12	10	~	4	4	N	12	12	13	4	N	N	δ	10	12	N	~	12	2	m	m	4	~	~	S	
336	486	336	336	336	729	366	390	1749	381	768	315	336	339	339	749	1611	342	336	339	339	685	819	336	336	
7.67	9.6	79.0	79.0	79.0	78.9	78.3	78.3	78.2	78.2	77.7	77.4	77.3	77.3	77.3	77.3	77.3	9.94	76.1	76.1	76.1	76.0	75.3	74.9	74.9	
315.8	315.2	312.8	312.8	312.8	312.6	310	310	309.8	309.6	307.8	306.6	306.2	306.2	306.2	306.2	306.2	303.2	301.4	301.4	301.4	301	298.2	296.6	296.6	
21	22	23	24	52	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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framework region;
                                                                  Murine 3D6 immunoglobulin light chain variable region DNA SEQ ID NO:1.
                                                                                                                                                                          partial
/note= "no stop codon given"
/product= "3D6 immunoglobulin light chain variable
                                                                                   ds; 3D6; light chain variable region; immunoglobulin; complementarity determining region; CDR; 10D5; variable framewor neuroprotective; nootropic; gene therapy; amyloidogenic disease; Alzheimer's disease.
                                                                                                                                                  Location/Qualifiers
                BP
                                                                                                                                                                                                                                                                                                              12-MAR-2003; 2003US-00388389.
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                ADR88405 standard; DNA; 396
                                                  (first entry)
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1. .60
/*tag= a
61. .393
/*tag= c
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*tag=
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                                  ADR88405;
RESULT 1
         ADR88405
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Yednock T;

Basi G, Saldanha JW, (NEUR-) NEURALAB LTD. (AMHP) WYETH.

WPI; 2004-668880/65.

05-NOV-2002 (first entry)

Claim 76; SEQ ID NO 1; 176pp; English N-PSDB; ADR88406 disease.

Sequence 396 BP; 101 A; 88 C; 99 G; 108 T; 0 U; 0 Other;

61 TATGTTGTGATGACCCCAGACTCCACTTTTGTCGGTTACCATTGGACAACCAGCCTCC 120 61 TATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 120 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGG 180 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGG 180 240 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 300 AGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTAGCTGGCAAGGTACACATTTTCCT 360 AGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT 360 9 9 TIGHTHACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAACTGGAC 1 Argardagrectecederrecretrrefrrageereregarreggaaaccaacegr ATGATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGT Gaps ö Length 396; 0; Indels ; Score 396; DB 13; ; Pred. No. 2.2e-119; 0; Mismatches 0; CGGACGTTCGGTGGAGCCACCAAGCTGGAAATCAAA 396 CGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 396 Query Match
Best Local Similarity 100.0%;
Matches 396; Conservative 0 301 301 121 121 181 181 241 361 361 엄 ઠ 유 ò g ò 셤 8 셤 ò g ò

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Gaps

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9 60 120 120 180 180 240 240 300 360

301 AGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT

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BP

ABS59426 standard; DNA; 384

ABS59426;

RESULT 2
ABS59426
ID ABS5
XX
AC ABS5

The present invention relates to new humanized immunoglobulin (Ig) light chain (LC) or heavy chain (HC) comprising variable region complementarity determining regions from 3D6/1005 Ig LC or HC variable region sequence, and variable framework region from human acceptor Ig LC or HC sequence. The invention is useful for preventing or treating an amyloidogenic floatease or Alzheimer's disease in a patient. The invention is also useful for in vivo imaging amyloid deposits in a patient. The present nucleic acid sequence encodes a mouse 3D6/10D5 variable light (VL) chain or 241 rerogadrecerdacaderreacrescadareacadeareacadarrrracaereanane 300 Mouse; humanized, immunoglobulin, 1g; light chain; LC; heavy chain; HC; variable region complementarity determining region; 3D6; 10D5; variable framework region; amyloidogenic disease; Alzheimer's disease; amyloid deposit; variable light chain; VL; variable heavy chain; VH; nootropic; neuroprotective; inhibitor of beta amyloid accumulation; 61 TATGTTGTGATGACCCCAGTCCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 121 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAAGAGAAGACATATTTGAATTGG 121 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGG 241 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 61 TATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCC Novel light/heavy chain of humanized immunoglobulin for treating amyloidogenic disease, has 3D6/10D5 variable region complementarity determining regions and variable framework region from human acceptor 1 ATGATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGT 1 ATGATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGT Length 384; Indels Sequence 384 BP; 95 A; 86 C; 97 G; 106 T; 0 U; 0 Other; variable heavy (VH) chain protein of the invention Score 384; DB 6; Le Pred. No. 1.9e-115; ö Query Match
97.0%; Score 384; up
Best Local Similarity 100.0%; Pred. No. 1.9
Matches 384; Conservative 0; Mismatches Claim 76; Page 79; 171pp; English. Yednock T; 06-DEC-2000; 2000US-0251892P. 06-DEC-2001; 2001WO-US046587. Saldanha J, (NEUR-) NEURALAB LTD 2002-519658/55 Mouse 3D6 VL gene WPI; 2002-519658, P-PSDB; ABG76923 Abeta; gene; ds. ımmunoglobulin WO200246237-A2 (AMHP) WYETH Mus musculus. 13-JUN-2002 181 Basi G, g 셤 셤 ઠે 셤 ઠે ð 셤 ò ઠે The invention relates to a novel humanised immunoglobulin light or heavy clain. The humanised immunoglobulin light or heavy chain comprises:

variable region complementarity determining regions (CDR's) from the 3D6 immunoglobulin light chain variable region sequence of 132 amino acids fully defined in the specification (ADR88406), or heavy chain variable region sequence of 131 amino acids fully defined in the specification (ADR88408), or from the 10D5 immunoglobulin light chain variable region sequence of 131 amino acids given in the specification (ADR88420), and a variable framework region from a cheavy chain variable region sequence of 142 amino acids fully defined in the specification (ADR88420); and a variable framework region from a cheavy chain variable region from a corresponding canno acid residue from the mouse 3D6 or 10D5 light or heavy chain corresponding amino acid residue from the mouse 3D6 or 10D5 light or heavy chain corresponding canno acid residue or aresidue participating in the VL-VH interface.

Con and may have a use in gene therapy. The composition and methods are useful for preventing or treating an amyloidogenic disease, such as Alzheimer's disease. The variable region sequence is useful in producing a three dimensional image of a 3D6 or 10D5 immunoglobulin immunoglobulin light chain variable region. New humanized antibodies that recognize beta amyloid peptides, useful for preventing or treating amyloidogenic diseases, such as Alzheimer's

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TRINH K.
WIMS L.
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ABN84610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a binding molecule which binds to human NogoA polypeptide, human NiG-D20 or human NogoA 623-640 with a dissociation constant of less than 1000nM. Also described. (1) a polynucleotide encoding the binding molecule; (2) an expression vector or system comprising the polynucleotide; (3) a host cell comprising the binding molecule and a carrier or diluent; and (5) treating the binding molecule and a carrier or diluent; and (5) treating diseases associated with nerve repair. The binding molecule has neuroprotective in preparing a composition for treating central nervous system (CNS) injury or neurodegenerative disorders. The present sequence encodes a mouse binding molecule 1107 light chain, which is used in the exemplification of the present invention.
New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding molecule; human; NogoA; NiG; NiG-D20; NogoA_623-640;
nerve repair; neuroprotective; gene therapy;
central nervous system injury; CNS injury; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;
Zurini M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 717;
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/*tag= a
/product= "binding molecule 11C7 light chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse binding molecule 11C7 light chain cDNA SEQ ID NO:44
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Pred. No. 6.3e-111;
0; Mismatches 14;
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                                                                                 361 CGGACGTTCGGTGGAGGCACCAAG 384
                                                                                                                                 361 cegacerreeregaecaccaae 384
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                                                                                                                                                                                                                                                                   ADP45590 standard; cDNA; 717
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Best Local Similarity 96.4%;
Matches 379; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS PHARMA GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-2002; 2002GB-00028832
                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mouse; gene; ss.
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                      123
                                   183
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9
                                                                            TCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAAAGACATATTTGAATTGGTTG
                                                                                                            244 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATCAGC
                                                                                                                                                                    241 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACGGATTTCACACTGAAAATCAGC
                                                                                                                                                                                                  304 AGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCTCGG
                      GTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCATC
                                                                                                                                                                                                                                                                                                                                                                                         Anti-Streptococcus mutans surface antigen MAb SWLA3 VL coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment and prevention of dental caries in mammals, in particular
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/product= "SWLA3 light chain variable region"
/note= "the CDS does not include a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen L,
                                                                                                                                                                                                                                             364 ACGITCGGTGGAGGCACCAAGCTGGAAATCAAA 396
                                                                                                                                                                                                                                                           361 ACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 393
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P-PSDB; ABB79729.
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ID ABZ
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                                                                                                               The present sequence is the coding sequence of the light chain variable region (VL) of the murine monoclonal antibody SWLA3 (IgG), which binds specifically to the surface antigons of cariogenic type of Streptococcus mutans (ATCC 25175). The coding sequence was obtained from SWLA3 (ATCC HB 12558) hybridoma cells by PCR amplification (see also ABN84626 and ABN84627). The SWLA3 VL and VH (see ABN84611) coding sequences were used in the preparation of chimeric monoclonal antibody TEFC comprising SWLA3 variable regions and human antibody constant regions. Such chimeric monoclonal antibodies can be used to prevent or treat dental caries in humans. The antibodies engage the effector apparatus of the human immune system when they bind cariogenic organisms, resulting in their destruction. The antibodies may be produced in edible plants, in transgenic animals, or in chicken eggs for oral ingestion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGGATCAGGGACAGATTTTACACTGAAAATC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGT
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humans by orally administering genetically engineered or purified antibodies that bind to surface antigens of carcinogenic organisms
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0
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Pred. No. 1.9e-110;
0; Mismatches 17; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 420 BP; 99 A; 98 C; 112 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGACGTTCGGTGGAGCCACCAAGCTGGAAATCAAA 396
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                                                                       Claim 7; Fig 3A; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.1%;
95.7%;
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64 GITGIGATGACCCAGACTCCACTCTTGTCGGTTACCATTGGACAACCAGCCTCCATC 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAAGAGAAAGACATATTTGAATTGGTTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATCAGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 AGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCTCGG 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AGAGTGGAGGCTGAGGATTTGGGAATTTATTATTGCTGGCAAGGTACACATTTTCCGCTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an antibody against the N terminus of glypican 3 (GPC3). The antiboduy can be used for causing cell disruption and can be uses as an anti-cancer agent. The present sequence represents a chimeric mouse-human antibody M3C11 light chain encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGAGTCCTGCCCAGTTCCTGTTAGTGCTCTGGATTCGGAAACCAACGGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 ATGAGICCIGCCCAGITCCTGTTTCTGTTAGICCTCTGGATTCGGGAAACCAACGGTTAI
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                                                                                                                                                                                                                                                                                                                                                                                                Ohizumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disruption and is useful as an anticancer agent.
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/*tag= a
/product= "M3C11 light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO 17; 122pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                Nakano K,
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AGCAGAGTCGAGGCTGAGGATGTGGGAGTTATTGCTGGCAAGGTACACATTTTCCT 360
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                            New humanized forms of mouse 3D6 antibodies, useful for treating Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGG
                                                                                                           TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC
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product= "Humanised antibody light chain"
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2. .408
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12. .1088
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P-PSDB; ABP58274.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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        Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanized forms of mouse 3D6 antibodies, useful for treating Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, or for inhibiting formation of or reducing Abeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TATGTTGTGATGACCCAGACTCCACTTTGTCGGTTACCATTGGACAACCAGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Argardagrecrecedagricerstricistragrecressarressaaaceaacear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                         /note= "the CDS does not include a stop codon"
1. .60
61. .717
/*tag= c
                                                                                                                                                                                                                                                                                                                                     /product= "Humanised 3D6 antibody light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 364; DB 8; Length 717;
Pred. No. 9.3e-109;
0; Mismatches 20; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 717 BP; 182 A; 185 C; 185 G; 165 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 12-13; 54pp; English.
                                                                                                                                                                                                                                                Location/Qualifiers
1. .717
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-2002; 2002WO-US011853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.9%;
Best Local Similarity 94.9%;
Matches 376; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-2001; 2001US-0287539P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIL ) LILLY & CO ELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plaque in the brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABP58274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200288306-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsurushita N,
                                                                                                                                             Mus sp.
Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mat_peptide
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                                                                                             gene; ss
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the present sequence is that of the gene, including an intron, encoding a humanised 3D6 light chain of the present invention. In the variable region of this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 3D6 and the framework region from human garmline Vk segment DRK19 and J segment JK4. Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 3D6 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed bost cells, and methods of using the humanised antibody to transformed prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain. (Updated on 27-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
amyloid angiopathy, or for inhibiting formation of or reducing Abeta
                                                                                  Claim 15; Page 15; 54pp; English
                                plague in the brain
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Yabuta N;

WPI; 1999-620204/53. P-PSDB; AAY52765. Sato K, Adachi H,

(CHUS) CHUGAI SEIYAKU

99WO-JP001768. 98JP-00091850

02-APR-1999; 03-APR-1998;

WO9951743-A1

Sequence 1953 BP; 548 A; 490 C; 384 G; 531 T; 0 U; 0 Other;

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61 TATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCC 120
                                                                                                                                                             72 GATGITGIGATGACCCCGGTCTCCCCTTGCCTGTTACCCTGGACAACCAGCCTCC 131
                                                                                                                                                                                                               132 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGG 191
                                                                                                                                                                                                                                                                                 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACACTGAAAATC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                          AGCAGAATAGAGGCTGAGGATTTGGGACTTTATTACTGGCAAGGTACACATTTTCCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 AGCAGAGTCGAGGCTGAGGATGTGGGAGTTTATTAGCTGGCAAGGTACACATTTTCCT 371
                                                                                                                                                                                                                                                                                                                  192 TriccaAcaccicaGccaGccaGrcrccaAGACGccraArcraTcrGGrGrcraAAcrGGAC 251
                                                                     9
                                                                                                      71
                                                                                         12 ATGATGAGTCCTGCCCAGTTCCTGTTTAGTGCTCTGGATTTCGGAAACCAACGGT
                                                                   1 ATGATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGT
                                    Gaps
                                    ö
Score 364; DB 8; Length 1953; Pred. No. 1.4e-108;
                                  20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGACGTTCGGTGGAGCCACCAAGCTGGAAATCAAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 cegacerrecerecaceaceaceaceacaaa 407
                                  0; Mismatches
 91.9%;
94.9%;
                                 Matches 376; Conservative
                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       241 '
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   Query Match
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Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
ATR-2; ATR-3; ATR-4; ATR-5; ATR-8; thrombotic disease; DIC;
disseminated intravascular coagulation; immunogenicity; chimeric; ss.
                                                                                                              Anti-tissue factor mouse monoclonal antibody ATR-7 L chain V region DNA.
                           AAZ33016 standard; DNA; 393
                                                                                  (first entry)
                                                                                   26-JAN-2000
                                                                                                                                                                                                    Synthetic.
Mus sp.
                                                        AAZ33016;
RESULT 8
               AAZ33016
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containing the variable region of the H chain of a mouse monoclonal Ab chain of a human tissue factor (hTF) and the constant region of the H chain of a mouse monoclonal Ab chain of a human Ab. The variable region is one of six specified sequences (which are the H chain variable regions from mouse monoclonal Ab s ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains or containing the variable region of the L chain of a mouse monoclonal Ab recognising human tissue factor (hTF) and the constant region of the L chain of a human Ab, the variable region being one of six specified cannot a human Ab, the variable regions from mouse monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment and prevention of thrombotic disease, especially of disseminated and prevention of thrombotic disease, especially of disseminated intravascular coaqulation (DIC). The humanised antibody has the high hTF binding activity of the mouse monoclonal antibody but greatly reduced immunogenicity. AAZ33001 to AAZ3301 and Y527007 to AAX52767 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 Griergergacceagacrecacreacrirergerraccarregacaaccaccecere 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 retreceascreasercasesceretrasarasesarasaasaasaararetraarrestre 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGGTTG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATCAGC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GITGIGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCATC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes chimeric antibody (Ab) heavy (H) chains
                                                                                                                                                                                                                                                                                                                                      Humanised antibody recognizing human tissue factor, used for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Argagrecrecederrecrerrrergradecreregarreggaareaacegrear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TTACAGAGGCCAGGCCACCAAAGCGCCTGATCTATCTTGTGTCTAAACTGGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGCACAGATTTCACACTGAAAATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.2%; Score 361; DB 2; Length 39 94.9%; Pred. No. 6.9e-108; ive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 393 BP; 98 A; 85 C; 104 G; 106 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 196-197; 291pp; Japanese
                                                                                                                                                                                                                                                                                                                                                       disseminated intravascular coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 94.9
Matches 373; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
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P-PSDB; AAR12361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                      25-MAR-2003
15-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9107493-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-1991.
                                                                                                                                                                                                                                                                          AAQ12063;
                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                AAQ12063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GTTGTACTGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCGTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 rcriscaagrcaagrcagagccrcrragaragrgarggaaagacararrrgaarrggrrg 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 GTTGTGATGACCCAGACTCCACTTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCATC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGGTTG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised antibody recognizing human tissue factor, used for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                             Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
disseminated intravascular coagulation; immunogenicity; chimeric; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                  Anti-tissue factor mouse monoclonal antibody ATR-8 L chain V region DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGGATTCGGGATATCAACGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 ATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogenicity. AAZ33001 to AAZ33091 and Y527007 to AAYS2767 re
sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 91.2%; Score 361; DB 2; Length 393; Best Local Similarity 94.9%; Pred. No. 6.9e-108; Matches 373; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 393 BP; 99 A; 85 C; 103 G; 106 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 197-198; 291pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disseminated intravascular coagulation.
             AAZ33017 standard; DNA; 393 BP.
                                                                                                                                                                                                                                                                                        99WO-JP001768.
                                                                                                                                                                                                                                                                                                                                                                             Sato K, Adachi H, Yabuta N;
                                                                                                                                                                                                                                                                                                                     98JP-00091850.
                                                                                                                                                                                                                                                                                                                                                (CHUS ) CHUGAI SEIYAKU KK.
                                                                     26-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-620204/53.
                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY52766
                                                                                                                                                                                                                                                                                        02-APR-1999;
                                                                                                                                                                                                                                                                                                                     03-APR-1998;
                                                                                                                                                                                                                                W09951743-A1
                                                                                                                                                                                                                                                             14-OCT-1999
                                                                                                                                                                                    Synthetic.
                                          AAZ33017;
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                                                                                                                                                                                                                                                                                              /*tag= a
/product= "mouse MAb 4D12 L(kappa)-chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New chimeric mouse-human antibodies - used to detect, kill and remove HIV
                                                                                                                                                                                                                                                      304 AGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCTCGG 363
241 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTCACACTGAAAATCAGC
                                                                                                            244 GGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence encoding light (kappa) chain variable region of murine 4D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 426 BP; 100 A; 99 C; 105 G; 122 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric antibodies; immunoconjugates; HIV; AIDS; ss.
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                                                                                                                                                                                                                                                                                                                                                                                            364 ACGITCGGTGGAGGCACCAAGCTGGAAATCAAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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(first entry)
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us-10-010-942b-1.rng

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The mouse VL gene product may be used to produce chimeric mouse- human Abs against HIV-1 comprising human Ig constant regions and murine variable regions. These novel sequence are useful in treatment, diagnosis and prophylaxis of HIV infections, and may be produced by a bacterial, yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                        330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; T-cell receptor; gene; cytostatic; dermatological; neuroprotective; immunostimulant; GD3; ganglioside antigen; MB3.6; FSM4; tumour; 3D8; 4D4; 3E11; prostate-specific membrane antigen; zeta signalling chain; CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer; heavy chain variable region; mouse.
                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                151 TTCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATTTTTGAATTGG 210
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                                                                                                                                                                                                                          90
                                                                                                                                                                                                                                                        61 TATGTTGTGATGACCCCAGTCCACTTTGTCGGTTACCATTGGACAACCAGCCTCC
                                                                                                                                                                                                                                                                                                                ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGG
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                                                                                                                                        Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse DNA encoding antibody 3D8 light chain variable region.
                                                                                                             Sequence 426 BP; 100 A; 99 C; 105 G; 122 T; 0 U; 0 Other;
                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 Arcacerregerecregeaccaaecragaacreaga 426
                                                                                                                                        Score 360.8; DB 2;
Pred. No. 8.3e-108;
                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 CGGACGTTCGGTGGAGCCACCAAGCTGGAAATCAAA
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                                                                                                                                                                     0; Mismatches
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                                                                                                                                         Query Match
Best Local Similarity 94.4%;
Matches 374; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABX16570 standard; DNA; 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New chimeric mouse human antibodies - used in treatment, diagnosis and prophylaxis of HIV infections.
                                                                                                                                91 GATGTTGTGATGACCCAGACTCCACTTTGTCGGTTACCATTGGACAACCAGCCTCC
                                                                                                                                                                                        TTCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGAAGACATTTTTGAATTGG
                                                                                                             61 TATGTTGTGATGACCCCAGACTCCACTTTGTCGGTTACCATTGGACAACCAGCCTCC
                                                                                                                                                                       ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGG
                                                                                                                                                                                                                               TICITIACAGAGGCCAGCCCAGTCTCCAAAGCGCCTTACTCTATCTGGTGTCTAAACTGGAC
                                                                                                                                                                                                                                                                                    TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGGATCAGGGACAGATTTTACACTGAAAATC
                                                                                                                                                                                                                                                                                                                                            AGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT
                                                                           AIGAIGAGICCIGCCCAGIICCIGIIICIGIIAGIGCICIGGAIICGGGAAACCAACGI
                                                        1 ATGATGAGTCCTGCCCAGTTCCTGTTTCTGTTAGTGCTCTGGATTCGGGAAACCAACGGT
                            Gaps
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0
Length 426;
                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoding mouse MAb 4D12 L chain V region.
Score 360.8; DB 2;
Pred. No. 8.3e-108;
                                                                                                                                                                                                                                                                                                                                                                                                   CGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robinson
                                                                                                                                                                                                                                                                                                                                                                                                                              391 Arcacerrederecredeaccaaecragaacreaa
              Pred. No. 8.3e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ghoshdasti P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
31. .426
/*tag= a
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91.1%;
94.4%;
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                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ12019 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Better MD, Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-1; chimera; ds
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (XOMA ) XOMA CORP.
(GREC ) GREEN CROS
(ZOMA-) ZOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR12239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1989;
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                         Matches 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
19-AUG-1991
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 Query Match
                Local
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Chimeric monoclonal antibodies - contain anti-human fibrin antibody light and heavy chain variable and constant for treating thrombotic conditions e.g. myocardial infarction.
                                                       Sequence of the chimeric kappa chain cDNA (1gkv) contained in pTB1427
                                                                                    Chimeric monoclonal antibody; anti-fibrin antibody; primer; antithrombotic agent; myocardial infarction therapy; 88.
                                                                                                                                                                                                                                                                                /*tag= c
/product= "C-kappa"
                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                     /*tag= b
/product= "V-kappa"
                                                                                                                                                                                         '*tag= a
'label= leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [wasa S, Tada H, Watanabe T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sxample; Fig 9; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                90JP-00413829.
91JP-00294464.
                                                                                                                                                                                                                                                                                                                                                                                    91EP-00121591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  st.1%;
sl Similarity 91.9%;
364; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TAKE ) TAKEDA CHEM IND LTD.
               (revised)
(first entry)
                                                                                                                                                                                                                                                                 134. .731
                                                                                                                                                                                                                      .410
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Best Local Similarity
Matches 364; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-209528/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR24811.
                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1991;
               25-MAR-2003
28-DEC-1992
                                                                                                                                                                                                                                                                                                                                                        24-JUN-1992.
                                                                                                                                                               Key
sig_peptide
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                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                            The invention relates to a chimaeric molecule comprising the GD3

(ganglioside antigen) binding domain of antibody MB3.6, with any of 3

(variable gene sequences, or the PSMA (prostate-specific membrane antigen)

binding domain of antibody 3D8, 4D4 and 3181, with variable gene

contained the zeta signalling chain of the T cell receptor and an

intervening CD8alpha hinge in which cysteine residues have been mutated.

The chimaeric molecules expressed in T cells or NK cells or other

the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),

the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),

and/or together with each other or with heterologous constructs to engage
additional stimulatory and functional properties of the effector cells to

enhance the antitumour therapeutic efficacy (claimed). They are

constructed antitumour sharpeutic efficacy (claimed) they are

tumours and prostate and small cell lung cancer. The present sequence

concept the mouse antibody 3D8 light chain variable region
                                                                                                                                                         New chimeric molecule useful in treating patients with disorders, such as melanoma, neuroendocrine disorders, prostate and small cell lung cancer comprises GD3 and/or PSMA binding domains of antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313 GCAGAGTGGAGGTGAGGATTTGGGAGTTTATTACTGCGTGCAAGGTACACATTTTCCTC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 TCTCTTGCAAGTCAAGTCAGAGCCTCTTATATAGTAATGGAAAAACCTATTTGAATTGGT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 CTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGAACAGATTTTACACTGAAATCA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCTC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTTGTGATGACCCAGACTCCACTCACTTTGTCGGTTACCATTGGACAACCAGCCTCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGAAGGAAAGACATATTTGAATTGGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATCA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TGATGAGTCCTGCCCAGTTCCTGTTTGTGTGCTCTGGATTCGGGAAACCAACGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 729 BP; 203 A; 177 C; 172 G; 177 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 ACACGTTCGGAGGGGGACCAAGCTGGAAATAAAA 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ25691 standard; cDNA; 737 BP
                                                                                                                                                                                                                     Claim 2; Fig 4E; 35pp; English.
               30-NOV-2000; 2000US-0250087P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 94.4%;
Matches 373; Conservative
                                                        (JUNG/) JUNGHANS R P.
                                                                                                                 WPI; 2003-208946/20.
                                                                                                                                P-PSDB; ABG74244,
                                                                                     Junghans RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
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Poly (A) + RNA was prepd. from the anti-fibrin chimeric Ab-producing transformant FIB1-H01/K63 and used as a template to clone human C-kappa chan using the oligo-dT (Pharmacia) primer as a primer for first etrand cDNA synthesis and the 3'E-kappa and 5'C-kappa primers for the PCR. An amplified DNA fragment of about 0.33kb was isolated and used to create a corresponding a cDNA contg. vector, PTB139. Using the same technique, with the 3'E-kappa primer as a primer for first strand synthesis and the 5'L-kappa and 3'C-kappa primer for the PCR, an anti-fibrin V-kappa primer for first strand synthesis and the 5'W-kappa and 3'W-kappa primer for first crand synthesis and the 5'W-kappa and 3'W-kappa primer for the PCR, an enti-fibrin V-kappa cDNA (V-kappa and 3'W-kappa primer for the PCR, and canti-fibrin V-kappa and 3'L-kappa and 3'C-kappa as a primer for first strand synthesis and the 5'S-kappa and 3'L-kappa cprimer for the PCR. The amplified gene fragments (L-kappa.v. V-kappa and 2'C-kappa and 3'L-kappa.v. V-kappa and 3'L-kappa.v. V-kappa and 2'C-kappa and 2
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Pred. No. 1.9e-102;
0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 737 BP; 186 A; 187 C; 189 G; 175 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; ortostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid archritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'product= "Murine antibody 1D9 kappa light chain variable
                                                                                       121 ATCTCTTGCAAGTCAAGTCAGAGCCTCTTAGATAGTGGAAAGACATATTTGAATTGG 180
                                                                                                                                                                              192 TIGITIACAGAGGCCAGGCCAGTCTCCAAGGGGCCTAATCTATCTGGTGTCTAAACTGTAC 251
                                                                                                                                                                                                                                                                      TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGATTTTACACTGAAAATC 300
                                                                                                                                                                                                                                                                                                                  252 TCTGGAGTCCCTGACAGGTTCACTGGCAGTGGATCAGGGACAGCTTTCACACTGAAAATC 311
                                                                                                                                                                                                                                                                                                                                                               AGCAGAATAGAGGCTGAGGATTTGGGACTTTATTATTGCTGGCAAGGTACACATTTTCCT 360
                                                                                                                                                                                                                                                                                                                                                                                                       312 AACAGAGTGGAGGCTGAGGATTTGGGAGTTTATTGCTGGCAAGGTATACATTTTCCG 371
61 TATGTTGTGATGACCCAGACTCCACTCTTTGTCGGTTACCATTGGACAACCAGCCTCC 120
                                          72 GATATTCAGCTGGCCCAGACTCCACTCACTTTTCGGTTACCATTGGACAACCAGCCTTC 131
                                                                                                              ATCTCTTGCACGTCAAGTCAGACCTCTTAGATAGTGATAGAAAGACATATTTGAATTGG 191
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/*tag= c
/product= "Murine mature antibody 1D9 kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine antibody 1D9 kappa light chain variable region encoding DNA
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/note= "Encodes a part of the constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 CGGACGTTCGGTGGAGCCACCAAGCTGGAAATCAAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 TACACGTTCGGAGGGGGACCAAGCTGGTGATCAAA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= d
/note= "Encodes variable region"
391. .426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variable region"
52. .390
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/*tag=
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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), CC comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting a leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune con a therosclerosis and atherosclerosis, and for inhibiting restenosis.

CC artherogenesis and atherosclerosis, and in the manufacture of a cuterogenesis and atherosclerosis, and in the manufacture of a condicament for treating CCR-2 mediated disease. They are also useful for treating allersy, anaphylaxis, malignancy, chronic and acute of confinammenton, histamine and IgE-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory confinement in a mammal. Humanised antibodies are also useful for inhibiting associated with vascular intervention, including angioplasty and/or stent confining allyperplasia of a vessel in a mammal, and inhibiting confining litherosciated with vascular intervention. The present sequence is a murine DNA encoding contine and indepty or contine 
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                                                                                                                                                                                                                                                                                                                                                                                        Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
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                                                                                                                                                                       O'keefe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 426 BP; 104 A; 97 C; 114 G; 111 T; 0 U; 0 Other;
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Best Local Similarity 94.3%; Pred. No. 1.8e-99;
Matches 348; Conservative 0; Mismatches 21;
                                                                                                                                                                       Jones ST,
                                                                                                                                                                       Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Fig 22; 183pp; English.
03-FEB-2000; 2000US-00497625.
                                                                                      (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                            Larosa GJ, Horvath C,
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The invention relates to humanised immunoglobulin heavy and light chains which have specificity for the CC-chemokine receptor 2 (CCR2) and an immunoglobulin or its antigen binding fragment comprising the chains. The humanised immunoglobulin or its antigen binding fragment preferably comprises two heavy chains and two light chains. The humanised immunoglobulin and its heavy and light chains. The humanised diagnosis, prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the CCR2 polypeptide, such as inflammatory diseases, autoimmune disorders, graft rejection, HIV infection and atheroselerosis. This sequence represents DNA encoding a mouse immunoglobulin protein of the invention.
                                                                                                                                       Mouse; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2; CCZ; infilammatory disease; autoimmune disorder; graft rejection; HIV infection; atherosclerosis; antiimmatory; immunosuppressive; anti-HIV; virucide; antiarteriosclerotic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists, useful for diagnosing and/or treating inflammatory or autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 426 BP; 104 A; 97 C; 114 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 95; 128pp; English.
ADQ89317 standard; DNA; 426 BP
                                                                                                                                                                                                                                                                                                                                                                              19-OCT-2001; 2001US-0350166P.
26-JUN-2002; 2002US-0392364P.
17-OCT-2002; 2002US-00272899.
                                                                                                                                                                                                                                                                                                                                            10-DEC-2003; 2003US-00733563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for diagnosing and/or diseases, and HIV infection.
                                                                                                     Mouse immunoglobulin DNA #1.
                                                                   21-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'keefe T, Ponath P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-580175/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OKEE/) O'KEEFE T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PONA/) PONATH P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ADQ89324.
                                                                                                                                                                                                                                                                    US2004151721-A1.
                                                                                                                                                                                                                                    Mus musculus.
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                                   ADQ89317;
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CTGTTAGTGCTCTGGATTCGGGAAACCAACGGTTATGTTGTGATGACCCCAGACTCCACTC

87 78

Gaps .; 0

21; Indels

0; Mismatches

TTAGATAGTGATGGAAAGACATATTTGAATTGGTTGTTACAGAGGCCAGGCCAGTCTCCA 207

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208 AAGCGCCTAATCTATCTGGTGTCTAAACTGGACTCTGGAGTCCCTGACAGGTTCACTGGC 267

198

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319 GTTTATTATTGCTGCCAAGGTACACATTTTCCGTACACGTTCGGAGGGGGGGACCAAGCTG 378
                                                                                  AGTGGATCAGGGACAGATTTCACACTGAAAATCAGCAGAGTGGAGCCTGAGGATTTGGGA
                                                                                                                           328 CTTTATTATTGCTGCCAAGGTACACATTTTCCTCGGACGTTCGGTGGAGGCACCAAGCTG
                                                        268 AGTGGATCAGGGACAGATTTTACACTGAAAATCAGCAGAATAGAGGCTGAGGATTTGGGA
                                                                                                                                                                                                                                                                                         Search completed: September 26, 2005, 05:09:03
Job time : 397 secs
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Matches 348; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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(oldsu) Anola agog sinji

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

September 26, 2005, 05:48:07 Run on:

77; Search time 90 Seconds (without alignments) 751.049 Million cell updates/sec

US-10-010-942B-2

Title: Perfect score:

1 MMSPAQFLFLLVLWIRETNG........CWQGTHFPRTFGGGTKLEIK 132 Sequence:

1612378 segs, 512079187 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Data Даве

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		:	sapien	sapien	sapien	sapien	sapien	sapien	musculu	ulu	p 3 (sapien	sapien	sapien	sapien	sapien	շոլո	pien	շոլո	sapien	շոլո	sapien	sapien	ոլո	շոյո	շոյո	musculu	sapien	sapien	culu	pien	amil	culu
		ption	homo	рошо	homo	homo	homo	homo	mus 1	mus	mus .	homo	homo	ношо	homo	homo	mus musculu	homo sapien	mus musculu	homo	mus musculu	рошо	homo	mus musculu	mus musculu	mus musculu	mus	homo	homo	mus musculu		-	mus musculu
		Description	Q8tcd0	P06310	Q8nek0	Q6p491	091180	Q6pih6	P01631	Q65zc0	Q65zq7	P06309	P01617	P01614	P01615	P01616	P01630	P18135	Q61em8	P06314	P03976	Q6pi18	Q6gmv9	P01629	P01627	P01661	P01628	P18136	P06313	P01626	Q6p5s8	P01618	Q7ts98
SUMMAKIES	•	OI .	Q8TCD0	KV2F HUMAN	OBNEKO	Q6P491	Q9UL80	9н1490	KV2G MOUSE	<u> </u>	Q652Q7	KV2E HUMAN	KV2D HUMAN	KV2A_HUMAN	KV2B_HUMAN	KV2C HUMAN	KV2F MOUSE	KV3L_HUMAN	Q6LEM8	KV4C HUMAN	KV2E MOUSE	Q6PIL8	Q6GMV9	KV2D MOUSE	KV2B_MOUSE	KV31 MOUSE	KV2C_MOUSE	KV3M_HUMAN	KV4B HUMAN	KV2A_MOUSE	Q6P5S8	KV1_CANFA	Q7TS98
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		Match Length DB	239	133	239	239	114	240	113	219	248	117	113	115	113	112	113	129	112	134	113	236	235	112	120	131	113	129	133	112	236	108	236
d	Query	Match	73.8	73.4	68.1	68.1	64.2	63.8	62.7	62.1	61.4	60.3	60.0	59.9	59.8	56.3	56.1	55.8	55.1	55.0	54.9	54.6	54.3	54.0	54.0	54.0	53.9	53.9	53.9	53.3	53.3	52.5	52.4
		Score	511	508	471	471	444.5	441.5	434	430	425	417	415	414.5	414	389.5	388	386	381	380.5	380	377.5	376	374	374	373.5	373	373	373	369	368.5	363.5	362.5
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Pol664 mus musculu P06311 homo sapien P04207 homo sapien G6kD65 mus musculu P01665 mus musculu P01667 mus musculu P01667 mus musculu P01667 mus musculu P01667 mus musculu Q6pjf2 homo sapien P01670 mus musculu P01679 mus musculu Q66977 mus musculu Q86977 mus musculu Q86977 mus musculu
KV3L MOUSE KV3K HUMAN KV3H HUMAN G6KBGE KV3M MOUSE KV3M MOUSE KV3O MOUSE KV3C MOUSE
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51.0 51.0 51.0 51.0 50.0 50.0 50.0 50.0
358.5 359.5 357.5 357.5 357.5 357.5 357.5 348.5 347.5 347.5
6 6 6 6 7 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9

ALIGNMENTS

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MEDILINE-2288257. PubMed=12477932; DOI=10.1073/pnas.242603899; MEDILINE-2288257. PubMed=12477932; DOI=10.1073/pnas.242603899; Mediline-2288257. PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Chuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K., Altorine R.F., Jordan H., Moore T., Max S.I., Wang J., Heibe F., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Abramson R.D., Mullahy S.J., McKernan K.J., Malek J.M., Gay L.J., Hulyk S.W., A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A. Helton B., Ketteman M., Madan A., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mitchige M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., K. Todriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., R. Generation and initial analysis of more than 15,000 full-length human and some standard s
                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Straubberg R.;
Straubberg R.;
Submitted (FBE-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022362; AAI2362.1; -.
PIR; S22658; S22658.
PIR; S44095; S34095.
PIR; S40324; S40324.
PIR; S40324; S40324.
PIR; S42267; S42267.
                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                  239 AA.
                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_WC.
Pfam; PF07654; C1-set; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
                                                  PRELIMINARY;
                                                                                                                                                                                  Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01834; 117Z
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                  Q8TCD0
RESULT 1
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Length 133;

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133 133
133 AA; 14707 MW; 513CCAF3673009EE CRC64;
                                       Query Match
Best Local Similarity 73.5
Matches 97; Conservative
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SEQUENCE
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                                                                                                                                                                            61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
                                                                                                                                                                                         61 PQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKITRVEAEDVGVYFCMQGTHWP 120
                                                                                                                                                   9
                                                                                                                                          1 MRLPAQLIGILMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSTQSLVYSDGNTYLNW
                                                                                                                            1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

BEDLINES 86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                          Query Match 73.8%; Score 511; DB 2; Length 239; Best Local Similarity 72.7%; Pred. No. 2.6e-41; Matches 96; Conservative 18; Mismatches 18; Indels
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Complementarity-determining-3
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypochaetical protein.
SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                                                                                                                                     01-07N-1988 (Rel. 06, Created)
01-07N-1988 (Rel. 06, Last sequence update)
01-07L-1999 (Rel. 38, Last annotation update)
1g kappa chain V-II region RPMI 6410 precursor.
                                                                                                                                                                                                                                                                                                                133 AA.
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PTR, A01890; KZHURP.
HSSP, Q99M37; 119.1.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR00710; Ig-like.
INTERPRO; IPR00710; Ig-like.
INTERPRO; IPR00710; Ig-like.
INTERPRO; IPR00710; Ig-like.
INTERPRO; IPR00406; Ig-v.
PROSITE; PSS0435; IG-LIKE; I.
IMMUNO910bulin, V region; Signal.
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                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                             121 RTFGGGTKLEIK 132
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                                                                                                                                                                                                                                                                                                                STANDARD;
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TISSUE=Prostate;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Faingold B.A., Grouse L.H., Derge J.G.,

Ralausner R.D., Collins F.S., Wagner L., Schaefer C.P., Bhat N.K.,

RA Altechul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

R. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

R. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Rohas S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

R. Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Marra M.H., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                           61 FQQRFGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYCMQGTHWS 120
                                                                                                                                                                                                                                                                                                                      61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
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                                                                                                                                                                                                                                         1 MRLPAQLIGLIMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNW
                                                                                                                                                           1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
                                                                             Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                 ;
73.4%; Score 508; DB 1; Length 13
73.5%; Pred. No. 2.6e-41;
tive 16; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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PIR; $34091; $34091.
PIR; $40342; $40342.
PIR; $40342; $40342.
HSSP; PO1834; 1172.
INTERPORT IPRO07110; Ig-like.
INTERPORT IPRO03597; Ig-cl.
INTERPORT IPRO03596; Ig-MHC.
INTERPORT IPRO03596; Ig-MHC.
PÉRM; PRO7554; C1-8et; I.
SMART; SMO0406; IGV; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
Homo sapiens (Human).
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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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NON TER
SEQUENCE
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Best Local 8
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Q6PIH6
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                                                                                                                                                                   9
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                                                                                                                                                                                       1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
                                                                                                                               Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                 ;
                                                                                          68.1%; Score 471; DB 2; Length 239;
68.2%; Pred. No. 1.9e-37;
ive 19; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (DRC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC063599; AAH63599.1; -.
HSSP; P01837; 1KCU.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS05290; IG_MHC; UNKNOWN_1.
HYPOCHELical protein_
SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 AA
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InterPro; IPR003599; IG.
InterPro; IPR003597; IG_C1.
InterPro; IPR003506; IG_MHC.
InterPro; IPR003596; IG_V.
SMART; SM00409; IG; 2.
SMART; SM00409; IGc1; 1.
                                                                                                                             90; Conservative
                                                                                                                                                                                                                                                                                                                      121 RIFGGGIKLEIK 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein. Homo sapiens (Human).
                                                                                                          Best Local Similarity
Matches 90; Conserv
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TISSUE=Skin;
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                                                                                            Query Match
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                                                                                                                                                                                                                                                                                   5 AQLIGELMLWVPGSSGDIVMTQTPLSSPVTIGQPASISCRSSBSLLHSNGNTYLSWLHQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS
                                                                                                                                                                                                                                                         5 AQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQR
                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 114;
                                                                                                                                                     Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13, Indels
                                                                                                                                                                                                       19; Indels
SMART; SM00406; IGV; 1.
PROSITE; PSS0835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 AA; 12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                68.1%; Score 471; DB 2;
68.8%; Pred. No. 1.9e-37;
cive 21; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.2%; Score 444.5; DB 2
76.8%; Pred. No. 3.2e-35;
iive 12; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035034; AAD56270.1; -.
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PIR, S23638; S23638.

PIR, S34094; S34094.

PIR, S34095; S34096.

HSSP; P01625; ILWE.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                             Local Similarity 68.8% tes 88; Conservative
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125 QGTRVEIK 132
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MOUSE
              KV2G MOU
P01631;
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KV2G MOUSE
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                                                                                                                                                              MEDLINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
X Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausher R.D., Collins F.S., Wagger L., Shenmen C.M., Schuler G.D.,
A Lischul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heish F.,
A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninoi P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHF- 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.8%; Score 441.5; DB 2; Length 240; 66.2%; Pred. No. 1.4e-34; ive 17; Mismatches 27; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg_R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO34142, AAH34142.1; -.
HSSP; P01837; 1KBS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26234 MW; 188D4DD8BB781EC4 CRC64;
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                                        Last sequence update)
Last annotation update)
240 AA
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SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                            Created)
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; C1-8et; I.
                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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Query Match
Best Local Similarity 66.2.,
Best Local Similarity
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PRELIMINARY;
                                                                  Hypothetical protein.
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                                                                                  (Human)
                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                         NCBI_TaxID=9606;
                                                                                   Homo sapiens
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RESULT 7

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MEDLINE=96319505; PubMed=9768802;
Kipp B., Schlaak M., Becker W.M.;
"Cloning and expression of a recombinant mouse Fab-fragment
recognizing a defined linear epitope of Chironomus thummi thummi major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLNWYLQKAQQSPKLLIYKVSNRFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS
                                                                                                                                                                                                                                                                                                               Novotny J., Margolies M.N.;
"Amino acid sequence of the light chain variable region from a mouse anti-digoxin hybridoma antibody.";
Blochemistry 22:115-1158(1983).
-!- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma protein that binds digoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 GVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTHVPPTFGGGTKLEIK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Q99M37; 1191.
InterPro; IRR00310; Ig-like.
InterPro; IRR003596; Ig_v.
Pfam; PF00047; Ig' 1.
SMART; SM00406; IGv; 1.
PROSTER; PSS0835; IG_LIKE; 1.
Direct protein sequencing; Hybridoma; Immunoglobulin V region; Monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complementarity-determining-1. Framework-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pramework-3.
Complementarity-determining-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complementarity-determining-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 62.7%; Score 434; DB 1; Length 11. Similarity 75.7%; Pred. No. 3.3e-34; 84; Conservative 11; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Framework-1.

Specification of Pramework-1.

Complementarity-determining-
Framework-2.

Complementarity-determining-
Pramework-3.

Complementarity-determining-
Framework-4.

By similarity.

113

A; 12273 MW; F9F39CE949A84C2A CRC64;
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Last annotation update)
                                                               21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
113 AA.
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Mus musculus (Mouse).
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PRT;
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MEDLINE=83178921; PubMed=6404298;
                                                                                                            Ig kappa chain V-II region 26-10.
                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seg
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STANDARD;
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                                                                                                                                      Mus musculus (Mouse)
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197 GVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGSGTKLEIK 247
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SMART; SM00406; IGv;
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59
66
98 1
107 1
117 AA;
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KV2D HUMAN
ID KV2D_HUMAN
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KV2E HUMAN
ID KV2E HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92020904; PubMed=1924323;

MEDLINE=92020904; PubMed=1924323;

MEDLINE=92020904; PubMed=1924323;

MEDLINE=92020904; PubMed=1924323;

The British of a fingle-chain immunotoxin that causes complete a single-chain immunotoxin that causes complete regression of a human carcinoma in mice.";

In Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).

EMBL: S57990; AAB19971.2; -..

REMBL: S57990; AAB19971.2; -..

InterPro; IPR003599; Ig.

InterPro; IPR003599; Ig.

R InterPro; IPR003596; Ig.v.

R Pfam; PP00047; ig; 2.

R SMART; SM00409; IG; 2.

R SMART; SM00409; IG; 2.

R SMART; CARRES SM0409; IG; 2.

R PROS SMART; SM0409; IG; 2.

R PROS SMART; SM0409; IG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10095,
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                                                                                                                                                                                                                                                                                                                                                                                    62.1%; Score 430; DB 2; Length 219; 73.0%; Pred. No. 1.6e-33; ive 16; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                              219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
            Int. Arch. Allergy Immunol. 110:348-353(1996).
EMBL; 237499; CAA85724.1; -
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003597; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
InterPro; IPR003596; Ig.
Pfam; PF07654; Cl-set; I.
Fam; PF07654; Cl-set; I.
Fam; PR00407; IG.; I.
SWART; SW00409; IG. 2.
SWART; SW00406; IG.; IG.; I.
PROSTIE; PS00290; IG. IKE; 2.
PROSTIE; PS00290; IG. IKE; I.
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(TrEMBLrel. 28, I
(TrEMBLrel. 28, I
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B3(Fv)-PE40 (Frag
Name=B3(Fv)-PE40;
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25-0CT-2004
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                           01-JAN/1988 (Rel. 06, Created)
1-JAN/1988 (Rel. 06, Last sequence update)
15-UTL-1998 (Rel. 38, Last annotation update)
16-UTL-1999 (Rel. 38, Last annotation update)
17-UTL-1999 (Rel. 38, Last annotation update)
18 kappa chain V-II region GM607 precursor (Fragment).
19 kappa chain (Human).
19 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=84191506; PubMed=6125927;
Klobeck H.G., Solomon A., Zachau H.G.;
"Contribution of human V kappa II germ-line genes to light-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V-II region GM607.
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69.6%; Pred. No. 1.5e-32;
ive 17; Mismatches 18;
117 AA.
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GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; IG-like.
InterPro; IPR003596; IG-N
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PIR; A01889; KZHUGM.
HSSP; Q99M37; 1191.
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Emunoglobulin V region; Signal.
NOW TER <1
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STANDARD;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                           MEDLINE=68242259; PubMed=5586923;
Ig kappa chain V-II region Cum
              Homo sapiens (Human)
                                                     NCBI_TaxID=9606;
                                                                               SEQUENCE
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KV2B HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IVWTQSPLSLPVTPGEPASISCRSSQSLLHSDGFDYLNWYLQKPQQSPZLLIYALSNRAS
                                                                                                                                                                                                                                                      Terry W.D., Page D.L., Kimura S., Isobe T., Osserman B.F., Glenner G.G.;
Glenner G.G.;
Structural identity of Bence Jones and amyloid fibril proteins in a patient with plasma cell dyscrasia and amyloidosis.";
J. Clin. Invest. 52:1276-1281(1973).
-!- MISCELLANEOUS: The major amyloid protein appears to be identical with the Bence Jones protein isolated from the same patient.
-!- MISCELLANEOUS: This protein was isolated from the urine of a patient with plasma cell dyscrasia and amyloidosis.
-!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                              MEDIINE=74148480; PubMed=4596149;
Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
"Amino acid sequence of a kappa Bence Jones protein from a case of
                                                                            Bukaryota, Metazca, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, 099M37; II91.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Fam; PP00047; ig; 1.
SWART; SW00406; IGv; 1.
PR087TE; PS50835; IG_LIKE; 1.
Amyloid; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.0%; Score 415; DB 1; Length 113; 71.2%; Pred. No. 2.3e-32; rive 14; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity-determining-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12316 MW; 0C3C38F81F1843CA CRC64;
            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
IIG kappa chain V-II region TEW.
Homo sapiens (Human).
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                                                                                                                                                                                                                                SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW). MEDLINE-73166638; PubMed=4700495;
                                                                                                                                    SEQUENCE (BENCE-JONES PROTEIN TEW).
                                                                                                                                                                                       primary amyloidosis.";
Biochemistry 12:3763-3780(1973).
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hes 79; Conservative
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KV2A_HUMAN
ID KV2A_HI
AC P01614;
DT 21-JUL.
DT 21-JUL.
DT 05-JUL.
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(Rel. 44, Last annotation update)

KV2A HUMAN P01614; 21-JUL-1986 (21-JUL-1986 (05-JUL-2004 (

115 AA

STANDARD;

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                                                                                                                                                           "Molecular basis of antibody formation.";
Naturwissenschaften 56:195-205(1969).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riesen W.F., Jaton J.-C.;
"Variable region sequence of the light chain from a Waldenstroms IgM with specificity for phosphorylcholine.";
Blochemistry 15:3829-3831(1976).
-!- MISCELLANBOUS: This chain was isolated from a Waldenstrom's macroglobulin that binds phosphorylcholine.
PIR; A01886; K2HUFR.
HSSP; Q99M37; 1191.
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Hilschmann N.; "The complete amino acid sequence of Bence Jones protein {\tt Cum} (kappa-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 SGVPDRFTGSGSGTDFTLKISKIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                         Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
                                                                                                                                                                                                                                                                                                                                                                                      59.9%; Score 414.5; DB 1
72.3%; Pred. No. 2.6e-32;
ive 13; Mismatches 17
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ig kappa chain V-II region FR.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-V.
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                                                                                                 REVISIONS TO 50; 52; 96 AND 97.
MEDLINE=70063440; PubMed=4188189;
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MEDLINE=76253627; PubMed=821524;
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nes 81; Conservative
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HSSP; P01751; 1NQB.
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; Pred. No. 6.6e-30; 24; Mismatches 16; Indels

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70; Conservative
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"The genetic, molecular, and cellular basis of antibody formation:
some facts and a unifying hypothesis.";
Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
-!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
-!- MISCELLANEOUS: This is a Bence-Jones protein.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Complementarity-determining-1.
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Framework-4.
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                                                                      Immunoglobulin V region.
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21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
19-UUL-2004 (Rel. 44, Last annotation update)
19 kappa chain V-II region MIL.
                                                                                                                                                                                                                                                                                                                                                   112 AA
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         30; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
GO; GO:0003823; F:antigen binding; NAS. GO; GO:0006955; P:immune response; NAS.
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HSSP, Q99M37; 1191.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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SWART; SW00406; IGv; 1.
PROSITE; PS50815; IG_LIKE; 1.
Immunoglobulin V region.
                                      PEam; PF00047; ig; 1. SMART; SM00406; IGv; 1. PROSITE; PS50835; IG LIKE; 1.
                                                                       protein sequencing;
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Matches 77; Conservative
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56.3%; Score 389.5; DB 1; Length 112;

Query Match

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22 VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                   82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
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SMART; SM00406; IGv; 1.
PROSTIE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Hybridoma; Immunoglobulin V region;
Monoclonal antibody.
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                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) RAD-2004 (Appa chain V-II region 7534.1. Mus musculus (Mouse).
                                                                                                                                                                                           113 AA
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By similarity.
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P01630;
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